



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 164940

**TO: Sarvamangala Devi**  
**Art Unit: 1645**  
**Location: REM-3C18**  
**Serial Number: 10/606618**

**Wednesday, April 26, 2006**

**From: Beverly Shears**  
**Location: Biotech-Chem Library**  
**REM 1A54**  
**Phone: 571-272-2528**  
**beverly.shears@uspto.gov**

### Search Notes

Your queries have completed processing. You may access an electronic version via eDAN (SCORE) and /or <http://es/ScoreAccessWeb>.

#### Protein Sequence Searches – February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (uniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

#### Published Applications Database - November 2005

Published\_Applications Nucleic Acid and Published\_Applications Amino Acid database searches now generate two sets of results each. The Published\_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published\_Applications\_New databases; older published applications make up the Published\_Applications\_Main databases.

Searches run against Nucleic Acid Published\_Applications produce two sets of results, with the extensions **.rnpbm** (Published\_Applications\_NA\_Main) and **.rnpbn** (Published\_Applications\_NA\_New).  
Searches run against Amino Acid Published\_Applications produce two sets of results, with the extensions **.rapbm** (Published\_Applications\_AA\_Main) and **.rapbn** (Published\_Applications\_AA\_New).



**This Page Blank (uspto)**

184940

**Shears, Beverly**

**From:** Devi, Sarvamangala  
**Sent:** Tuesday, April 11, 2006 2:42 PM  
**To:** STIC-Biotech/ChemLib  
**Cc:** Shears, Beverly  
**Subject:** 10/606,618

Please ask Ms. Beverly Shears to perform this search.

In application 10/606,618, please perform a sequence search for an at least eight amino acid-long peptide of SEQ ID NO: 4 in commercial and pending application databases.

Thanx.

S. DEVI, Ph.D.  
 Primary Examiner  
 AU 1645  
 Rems - 3C18

2

Date completed: _____	Search Site	Vendors
Searcher: <u>Beverly e 2528</u>	_____ STIC	_____ IG
Terminal time: _____	_____ CM-1	_____ STN
Elapsed time: _____	_____ Pre-S	_____ Dialog
CPU time: _____	Type of Search	_____ APS
Total time: _____	_____ N.A. Sequence	_____ Geninfo
Number of Searches: _____	_____ A.A. Sequence	_____ SDC
Number of Databases: _____	_____ Structure	_____ DARC/Questel
	_____ Bibliographic	_____ Other <u>can</u>

**This Page Blank (uspto)**



GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 12, 2006, 16:23:33 ; Search time 48 Seconds  
(without alignments)  
1372.761 Million cells

**Title:** US-10-606-618-4

Perfect score: 79

Sequence: 1 MKLKOIASALMMLGISPLAF.....LKKKPEDEIQRFQFLGTTF 797

Scoring table: OLIGO

scoring cable: 0.000  
Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size : 1

Total number of hits satisfying chosen parameters: 566853

Minimum DB seq length: 0

Minimum DB seq length: 200000000  
Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : Issued Patents AA:\*

1: /cqn2 6/ptodata/1/iaa/5 COMB.pcp:\*

```
1: /cgnz_6/ptodata/1/iaa/6_COMB.pep.*
2: /cgnz_6/ptodata/1/iaa/6_COMB.pep.*
```

3: /cgn2\_6/ptodata/1/iaa/H\_COMB.per:\*

4: /cgn2\_6/prodata/1/iaa/PCTUS COMB.pcp:\*

5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep:\*

```
6: /cqn2_6/prodata/1/iaa/backfiles1.pep:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query %		Length	DB	ID	Description
		Match					
1	797	100.0	797	2	US-09-994-192-4		Sequence 4, Appli
2	157	19.7	792	2	US-09-994-192-2		Sequence 2, Appli
3	8	1.0	94	2	US-09-489-039A-8163		Sequence 8163, Ap
4	8	1.0	97	2	US-09-205-258-1092		Sequence 1092, Ap
5	8	1.0	97	2	US-10-004-860-1092		Sequence 1092, Ap
6	8	1.0	230	2	US-09-270-767-45805		Sequence 45805, A
7	8	1.0	274	2	US-09-502-540-15552		Sequence 15552, A
8	8	1.0	648	2	US-09-252-991A-24628		Sequence 24628, A
9	8	1.0	1589	2	US-09-543-681A-4998		Sequence 4998, Ap
10	7	0.9	23	2	US-09-674-973A-147		Sequence 147, App
11	7	0.9	58	2	US-08-971-089-10		Sequence 10, Appl
12	7	0.9	58	2	US-10-117-604A-10		Sequence 7231, Ap
13	7	0.9	60	2	US-09-513-999C-7231		Sequence 6352, Ap
14	7	0.9	86	2	US-09-328-352-6252		Sequence 10485, A
15	7	0.9	86	2	US-09-489-039A-10485		Sequence 325, App
16	7	0.9	88	2	US-09-461-325-325		Sequence 325, App
17	7	0.9	88	2	US-10-012-543-325		Sequence 325, App
18	7	0.9	87	2	US-10-115-123-325		Sequence 18360, A
19	7	0.9	97	2	US-09-252-991A-18360		Sequence 62368, A
20	7	0.9	106	2	US-09-270-767-62368		Sequence 6601, Ap
21	7	0.9	110	2	US-09-513-999C-6601		Sequence 5037, Ap
22	7	0.9	129	2	US-09-543-681A-5037		Sequence 13, Appl
23	7	0.9	147	1	US-08-942-819-13		Sequence 21, Appl
24	7	0.9	147	2	US-09-522-955A-21		Sequence 7658, Ap
25	7	0.9	157	2	US-09-543-681A-7658		Sequence 39460, A
26	7	0.9	157	2	US-09-270-767-39460		Sequence 54677, A
27	7	0.9	157	2	US-09-270-767-54677		

101	7	0.9	544	2	US-09-383-912-10	Sequence 10, Appl	174	7	0.9	1434	2	US-09-724-631-10	Sequence 10, Appl
102	7	0.9	559	2	US-09-252-991A-24692	Sequence 24692, A	175	7	0.9	1434	2	US-08-954-701A-10	Sequence 10, Appl
103	7	0.9	568	2	US-09-949-016-10896	Sequence 10896, A	176	7	0.9	1434	2	US-09-754-032-10	Sequence 10, Appl
104	7	0.9	576	2	US-09-252-991A-23246	Sequence 23246, A	177	7	0.9	1434	2	US-08-916-140-10	Sequence 10, Appl
105	7	0.9	587	2	US-09-538-092-1130	Sequence 1130, Ap	178	7	0.9	1434	4	PCr-US95-13233-10	Sequence 10, Appl
106	7	0.9	604	2	US-09-345-473E-17	Sequence 17, Appl	179	7	0.9	1447	1	US-08-540-406-19	Sequence 19, Appl
107	7	0.9	604	2	US-09-862-027-17	Sequence 17, Appl	180	7	0.9	1447	2	US-08-656-055-19	Sequence 19, Appl
108	7	0.9	609	2	US-09-311-021-196	Sequence 196, App	181	7	0.9	1447	2	US-08-954-668-19	Sequence 19, Appl
109	7	0.9	614	2	US-09-328-352-4504	Sequence 4504, Ap	182	7	0.9	1447	2	US-09-268-140-5	Sequence 5, Appl
110	7	0.9	620	1	US-08-484-105-4	Sequence 4, Appli	183	7	0.9	1447	2	US-08-918-658-19	Sequence 19, Appl
111	7	0.9	620	1	US-08-484-105-4	Sequence 4, Appli	184	7	0.9	1447	2	US-09-724-631-19	Sequence 19, Appl
112	7	0.9	621	2	US-09-252-991A-19125	Sequence 19125, A	185	7	0.9	1447	2	US-08-954-701A-19	Sequence 19, Appl
113	7	0.9	671	2	US-08-858-207A-301	Sequence 301, App	186	7	0.9	1447	2	US-09-807-007-6	Sequence 6, Appli
114	7	0.9	671	2	US-09-583-110-3642	Sequence 3642, Ap	187	7	0.9	1447	2	US-09-754-032-19	Sequence 19, Appl
115	7	0.9	676	2	US-09-107-433-4098	Sequence 4098, Ap	188	7	0.9	1447	2	US-08-916-140-19	Sequence 19, Appl
116	7	0.9	699	1	US-08-694-865-16	Sequence 16, Appl	189	7	0.9	1447	4	PCr-US95-13233-19	Sequence 19, Appl
117	7	0.9	699	2	US-09-124-491-16	Sequence 16, Appl	190	7	0.9	1449	2	US-09-303-518D-652	Sequence 652, App
118	7	0.9	699	2	US-09-383-912-16	Sequence 16, Appl	191	7	0.9	1454	2	US-09-673-896-2	Sequence 2, Appli
119	7	0.9	699	2	US-09-252-991A-17073	Sequence 17073, A	192	7	0.9	1457	2	US-09-673-896-4	Sequence 4, Appli
120	7	0.9	783	2	US-09-248-796A-15502	Sequence 15502, A	193	7	0.9	1457	2	US-09-303-518D-650	Sequence 650, App
121	7	0.9	821	2	US-09-252-991A-21013	Sequence 21013, A	194	7	0.9	1468	2	US-09-303-518D-654	Sequence 654, App
122	7	0.9	827	2	US-09-543-681A-6425	Sequence 6425, Ap	195	7	0.9	1633	2	US-09-902-540-12892	Sequence 12892, A
123	7	0.9	901	2	US-09-270-767-45367	Sequence 45367, A	196	7	0.9	1686	2	US-09-355-160D-2	Sequence 2, Appli
124	7	0.9	908	2	US-08-714-741-44	Sequence 44, Appl	197	7	0.9	1686	2	US-10-092-219-2	Sequence 2, Appli
125	7	0.9	924	2	US-08-619-812-8	Sequence 8, Appli	198	7	0.9	2431	1	US-07-920-281C-2	Sequence 2, Appli
126	7	0.9	926	1	US-07-908-253-2	Sequence 2, Appli	199	7	0.9	2431	2	US-08-466-277-2	Sequence 2, Appli
127	7	0.9	926	1	US-08-455-970A-2	Sequence 2, Appli	200	7	0.9	2431	2	US-09-688-842-2	Sequence 2, Appli
128	7	0.9	926	1	US-08-387-156-6	Sequence 6, Appli	201	7	0.9	3122	2	US-10-237-551-201	Sequence 201, App
129	7	0.9	926	1	US-08-694-865-6	Sequence 6, Appli	202	7	0.9	3122	2	US-10-237-551-250	Sequence 250, App
130	7	0.9	926	1	US-08-878-748-6	Sequence 6, Appli	203	6	0.8	7	1	US-08-384-680-2	Sequence 2, Appli
131	7	0.9	926	1	US-08-535-837-2	Sequence 2, Appli	204	6	0.8	7	1	US-08-384-680-12	Sequence 12, Appl
132	7	0.9	926	2	US-09-124-491-6	Sequence 6, Appli	205	6	0.8	9	1	US-08-986-234-84	Sequence 84, Appl
133	7	0.9	926	2	US-09-383-912-6	Sequence 6, Appli	206	6	0.8	10	1	US-08-397-101-7	Sequence 7, Appli
134	7	0.9	926	2	US-08-976-566-2	Sequence 2, Appli	207	6	0.8	10	2	US-08-135-319A-4	Sequence 4, Appli
135	7	0.9	926	6	5476657-3	Patent No. 5476657	208	6	0.8	10	2	US-08-135-319A-5	Sequence 5, Appli
136	7	0.9	934	1	US-08-215-805A-80	Sequence 80, Appl	209	6	0.8	10	2	US-08-135-319A-6	Sequence 6, Appli
137	7	0.9	936	1	US-08-455-970A-12	Sequence 12, Appl	210	6	0.8	10	2	US-08-135-319A-19	Sequence 19, Appl
138	7	0.9	936	2	US-08-976-566-12	Sequence 12, Appl	211	6	0.8	10	4	PCr-US93-08436-7	Sequence 7, Appli
139	7	0.9	943	1	US-08-455-970A-10	Sequence 10, Appl	212	6	0.8	13	1	US-08-803-899-13	Sequence 13, Appl
140	7	0.9	943	2	US-08-976-566-10	Sequence 10, Appl	213	6	0.8	14	2	US-10-312-691-6	Sequence 6, Appli
141	7	0.9	951	1	US-08-455-970A-14	Sequence 14, Appl	214	6	0.8	18	1	US-08-279-058B-20	Sequence 20, Appl
142	7	0.9	951	2	US-08-976-566-14	Sequence 14, Appl	215	6	0.8	18	2	US-08-828-323-20	Sequence 20, Appl
143	7	0.9	963	2	US-09-914-259-20	Sequence 20, Appl	216	6	0.8	18	2	US-08-828-323A-20	Sequence 20, Appl
144	7	0.9	963	2	US-09-914-259-20	Sequence 20, Appl	217	6	0.8	19	1	US-08-634-060-42	Sequence 42, Appl
145	7	0.9	963	2	US-09-538-092-1060	Sequence 1060, Ap	218	6	0.8	19	2	US-08-676-186-1	Sequence 1, Appli
146	7	0.9	970	1	US-09-538-092-1060	Sequence 1060, Ap	219	6	0.8	19	2	US-09-932-923-1	Sequence 1, Appli
147	7	0.9	977	1	US-08-248-796A-16191	Sequence 16191, A	220	6	0.8	20	1	US-08-279-906A-22	Sequence 22, Appl
148	7	0.9	977	1	US-08-387-156-8	Sequence 8, Appli	221	6	0.8	24	2	US-09-843-221A-129	Sequence 129, App
149	7	0.9	977	1	US-08-694-865-8	Sequence 8, Appli	222	6	0.8	24	2	US-09-843-221A-130	Sequence 130, App
150	7	0.9	977	1	US-08-878-748-8	Sequence 8, Appli	223	6	0.8	25	2	US-09-911-927-35	Sequence 35, Appl
151	7	0.9	977	2	US-09-124-491-8	Sequence 8, Appli	224	6	0.8	25	2	US-09-911-882-35	Sequence 35, Appl
152	7	0.9	978	2	US-09-383-912-8	Sequence 8, Appli	225	6	0.8	25	2	US-09-911-888-35	Sequence 35, Appl
153	7	0.9	978	2	US-09-949-016-10196	Sequence 10196, A	226	6	0.8	26	2	US-08-965-762-35	Sequence 35, Appl
154	7	0.9	979	2	US-09-303-518D-648	Sequence 648, App	227	6	0.8	26	2	US-08-433-522A-35	Sequence 35, Appl
155	7	0.9	1022	1	US-09-949-016-10242	Sequence 10242, A	228	6	0.8	27	2	US-09-135-166-35	Sequence 35, Appl
156	7	0.9	1069	1	US-07-777-715-9	Sequence 9, Appli	229	6	0.8	27	2	US-08-942-046-35	Sequence 35, Appl
157	7	0.9	1069	1	US-08-170-126-4	Sequence 4, Appli	230	6	0.8	28	1	US-08-724-774B-4	Sequence 4, Appli
158	7	0.9	1098	1	US-08-954-418-4	Sequence 4, Appli	231	6	0.8	28	2	US-09-089-595-4	Sequence 4, Appli
159	7	0.9	1098	1	US-07-777-715-7	Sequence 7, Appli	232	6	0.8	28	2	US-09-382-855-4	Sequence 4, Appli
160	7	0.9	1098	1	US-08-170-126-2	Sequence 2, Appli	233	6	0.8	28	2	US-09-183-714B-4	Sequence 4, Appli
161	7	0.9	1098	2	US-08-954-418-2	Sequence 2, Appli	234	6	0.8	28	2	US-09-642-281-4	Sequence 4, Appli
162	7	0.9	1121	2	US-08-915-048A-2	Sequence 2, Appli	235	6	0.8	28	2	US-09-589-717-4	Sequence 4, Appli
163	7	0.9	1129	2	US-09-252-991A-28552	Sequence 28552, A	236	6	0.8	28	2	US-09-843-221A-93	Sequence 93, Appl
164	7	0.9	1296	2	US-08-857-636-60	Sequence 60, Appl	237	6	0.8	28	2	US-09-843-221A-94	Sequence 94, Appl
165	7	0.9	1334	6	5476657-1	Patent No. 5476657	238	6	0.8	30	2	US-09-471-276-1203	Sequence 1203, Ap
166	7	0.9	1403	1	US-07-908-253-3	Sequence 3, Appli	239	6	0.8	30	2	US-09-843-221A-124	Sequence 124, App
167	7	0.9	1403	1	US-08-694-865-17	Sequence 17, Appl	240	6	0.8	30	2	US-09-843-221A-125	Sequence 125, App
168	7	0.9	1403	2	US-08-535-837-3	Sequence 3, Appli	241	6	0.8	30	2	US-09-843-221A-158	Sequence 158, App
169	7	0.9	1403	2	US-09-124-491-17	Sequence 17, Appl	242	6	0.8	31	2	US-09-228-990-50	Sequence 50, Appl
170	7	0.9	1434	1	US-08-383-912-17	Sequence 17, Appl	243	6	0.8	33	1	US-08-209-747-19	Sequence 19, Appl
171	7	0.9	1434	1	US-08-540-406-10	Sequence 10, Appl	244	6	0.8	33	1	US-08-458-298-19	Sequence 19, Appl
172	7	0.9	1434	2	US-08-656-055-10	Sequence 10, Appl	245	6	0.8	34	1	US-07-915-247A-23	Sequence 23, Appl
173	7	0.9	1434	2	US-08-954-668-10	Sequence 10, Appl	246	6	0.8	34	1	US-08-443-863-23	Sequence 23, Appl

247	6	0.8	34	1	US-08-448-070-23	Sequence 23, Appl	320	6	0.8	74	2	US-09-248-796A-25832	Sequence 25832, A
248	6	0.8	34	1	US-08-449-500-23	Sequence 23, Appl	321	6	0.8	74	2	US-09-513-999C-5011	Sequence 5011, Ap
249	6	0.8	34	1	US-08-449-317A-23	Sequence 23, Appl	322	6	0.8	75	2	US-09-252-991A-21927	Sequence 21927, A
250	6	0.8	34	1	US-08-449-022-23	Sequence 23, Appl	323	6	0.8	75	2	US-09-198-452A-1228	Sequence 1228, Ap
251	6	0.8	34	1	US-08-449-447-23	Sequence 23, Appl	324	6	0.8	75	2	US-09-270-767-33600	Sequence 33600, A
252	6	0.8	34	1	US-08-184-328-23	Sequence 23, Appl	325	6	0.8	75	2	US-09-270-767-48817	Sequence 48817, A
253	6	0.8	34	1	US-08-521-097-23	Sequence 23, Appl	326	6	0.8	76	2	US-09-621-976-6191	Sequence 6191, Ap
254	6	0.8	34	1	US-08-843-221A-88	Sequence 88, Appl	327	6	0.8	78	2	US-09-732-210-1591	Sequence 1591, Ap
255	6	0.8	34	2	US-08-843-221A-89	Sequence 89, Appl	328	6	0.8	79	2	US-09-270-767-39286	Sequence 39286, A
256	6	0.8	34	2	US-08-843-221A-122	Sequence 89, Appl	329	6	0.8	79	2	US-09-270-767-54503	Sequence 54503, A
257	6	0.8	34	2	US-08-903-124-23	Sequence 122, App	330	6	0.8	80	1	US-08-209-747-12	Sequence 12, Appl
258	6	0.8	34	2	US-09-902-540-14017	Sequence 23, Appl	331	6	0.8	80	1	US-08-458-298-12	Sequence 12, Appl
259	6	0.8	36	2	US-08-751-344B-18	Sequence 14017, A	332	6	0.8	80	1	US-08-710-749-18	Sequence 18, Appl
260	6	0.8	39	1	US-08-209-747-23	Sequence 18, Appl	333	6	0.8	80	2	US-09-336-536-35	Sequence 35, Appl
261	6	0.8	39	1	US-08-458-298-23	Sequence 23, Appl	334	6	0.8	80	2	US-09-147-875A-19	Sequence 19, Appl
262	6	0.8	39	2	US-09-270-767-31845	Sequence 23, Appl	335	6	0.8	80	2	US-09-640-211A-905	Sequence 905, App
263	6	0.8	40	2	US-09-270-767-47062	Sequence 31845, A	336	6	0.8	82	2	US-09-134-001C-2951	Sequence 2951, Ap
264	6	0.8	42	4	PCT-US96-10043-13	Sequence 47062, A	337	6	0.8	84	2	US-09-621-976-5976	Sequence 5976, Ap
265	6	0.8	47	1	US-08-209-747-24	Sequence 13, Appl	338	6	0.8	84	2	US-09-270-767-32345	Sequence 32345, A
266	6	0.8	47	1	US-08-209-747-26	Sequence 24, Appl	339	6	0.8	84	2	US-09-270-767-46371	Sequence 46371, A
267	6	0.8	47	1	US-08-458-298-24	Sequence 26, Appl	340	6	0.8	84	2	US-09-270-767-47562	Sequence 47562, A
268	6	0.8	47	1	US-08-458-298-26	Sequence 24, Appl	341	6	0.8	84	2	US-09-311-021-100	Sequence 100, App
269	6	0.8	48	1	US-08-209-747-21	Sequence 26, Appl	342	6	0.8	84	2	US-09-513-999C-5815	Sequence 5815, Ap
270	6	0.8	48	1	US-08-458-298-21	Sequence 21, Appl	343	6	0.8	86	1	US-08-680-726A-82	Sequence 82, Appl
271	6	0.8	48	1	US-08-209-747-30	Sequence 22, Appl	344	6	0.8	86	2	US-09-092-409-82	Sequence 34956, A
272	6	0.8	49	1	US-08-209-747-22	Sequence 22, Appl	345	6	0.8	86	2	US-09-270-767-50173	Sequence 50173, A
273	6	0.8	49	1	US-08-458-298-22	Sequence 22, Appl	346	6	0.8	86	2	US-09-543-681A-7373	Sequence 7373, Ap
274	6	0.8	50	1	US-08-209-747-27	Sequence 27, Appl	347	6	0.8	87	2	US-09-270-767-32832	Sequence 32832, A
275	6	0.8	51	1	US-08-458-298-27	Sequence 20, Appl	348	6	0.8	87	2	US-09-270-767-48049	Sequence 48049, A
276	6	0.8	51	1	US-08-209-747-20	Sequence 30, Appl	349	6	0.8	88	2	US-09-489-039A-10714	Sequence 10714, A
277	6	0.8	51	1	US-08-209-747-30	Sequence 30, Appl	350	6	0.8	88	2	US-09-687-637B-29	Sequence 29, Appl
278	6	0.8	51	1	US-08-458-298-20	Sequence 30, Appl	351	6	0.8	89	2	US-09-687-637B-30	Sequence 30, Appl
279	6	0.8	51	1	US-08-458-298-30	Sequence 30, Appl	352	6	0.8	89	2	US-08-209-747-16	Sequence 16, Appl
280	6	0.8	52	2	US-09-277-078-46	Sequence 26, Appl	353	6	0.8	90	1	US-08-458-298-16	Sequence 16, Appl
281	6	0.8	55	1	US-08-209-747-25	Sequence 45, Appl	354	6	0.8	90	2	US-09-621-976-4742	Sequence 4742, Ap
282	6	0.8	55	1	US-08-458-298-25	Sequence 25, Appl	355	6	0.8	96	2	US-09-107-532A-6122	Sequence 6122, Ap
283	6	0.8	56	2	US-08-936-165A-332	Sequence 332, App	356	6	0.8	98	2	US-09-147-875A-1	Sequence 1, Appl
284	6	0.8	56	2	US-09-621-976-5925	Sequence 5925, Ap	357	6	0.8	98	2	US-09-147-875A-9	Sequence 9, Appl
285	6	0.8	56	2	US-09-270-767-57982	Sequence 57982, A	358	6	0.8	99	1	US-08-710-749-10	Sequence 10, Appl
286	6	0.8	57	2	US-09-006-428A-5	Sequence 57982, A	359	6	0.8	99	1	US-08-710-749-10	Sequence 10, Appl
287	6	0.8	57	2	US-09-615-387C-5	Sequence 57771, A	360	6	0.8	99	1	US-08-710-749-11	Sequence 11, Appl
288	6	0.8	58	2	US-09-270-767-57771	Sequence 57771, A	361	6	0.8	99	2	US-09-732-210-1583	Sequence 11, Appl
289	6	0.8	59	2	US-09-621-976-6937	Sequence 6937, Ap	362	6	0.8	99	2	US-09-147-875A-11	Sequence 14, Appl
290	6	0.8	59	2	US-09-270-767-61138	Sequence 61138, A	363	6	0.8	99	2	US-09-147-875A-14	Sequence 15, Appl
291	6	0.8	60	2	US-08-928-213B-70	Sequence 70, Appl	364	6	0.8	99	2	US-09-147-875A-15	Sequence 16, Appl
292	6	0.8	61	2	US-09-248-796A-25960	Sequence 25960, A	365	6	0.8	99	2	US-09-147-875A-16	Sequence 19, Appl
293	6	0.8	61	2	US-09-248-796A-24801	Sequence 24801, A	366	6	0.8	100	1	US-08-308-494A-19	Sequence 4, Appl
294	6	0.8	61	2	US-09-248-796A-26402	Sequence 26402, A	367	6	0.8	100	2	US-09-147-875A-8	Sequence 8, Appl
295	6	0.8	63	2	US-09-673-395A-403	Sequence 403, App	368	6	0.8	100	2	US-09-147-875A-10	Sequence 12, Appl
296	6	0.8	64	1	US-08-209-521-20	Sequence 20, Appl	369	6	0.8	100	2	US-09-147-875A-12	Sequence 3, Appl
297	6	0.8	64	2	US-08-961-810-130	Sequence 130, App	370	6	0.8	101	1	US-08-710-749-3	Sequence 7, Appl
298	6	0.8	64	2	US-08-352-902D-130	Sequence 130, App	371	6	0.8	101	1	US-08-710-749-7	Sequence 9, Appl
299	6	0.8	64	2	US-09-265-503B-130	Sequence 130, App	372	6	0.8	101	2	US-09-147-875A-9	Sequence 1, Appl
300	6	0.8	64	2	US-09-270-767-61944	Sequence 61944, A	373	6	0.8	101	2	US-08-169-701-1	Sequence 1, Appl
301	6	0.8	65	2	US-09-248-796A-25471	Sequence 25471, A	374	6	0.8	102	1	US-08-710-749-8	Sequence 8, Appl
302	6	0.8	65	2	US-09-640-211A-604	Sequence 604, App	375	6	0.8	102	1	US-08-710-749-21	Sequence 21, Appl
303	6	0.8	65	2	US-09-621-976-4488	Sequence 4488, App	376	6	0.8	102	1	US-08-760-903-1	Sequence 1, Appl
304	6	0.8	66	2	US-09-270-767-60792	Sequence 60792, A	377	6	0.8	102	1	US-08-482-191-1	Sequence 1, Appl
305	6	0.8	67	2	US-09-248-796A-23279	Sequence 23279, A	378	6	0.8	102	2	US-09-147-875A-18	Sequence 18, Appl
306	6	0.8	68	2	US-09-252-991A-30574	Sequence 30574, A	379	6	0.8	102	2	US-09-270-767-57873	Sequence 57873, A
307	6	0.8	68	2	US-09-489-039A-11466	Sequence 11466, A	380	6	0.8	102	2	US-09-902-540-14676	Sequence 14676, A
308	6	0.8	68	2	US-09-902-540-11724	Sequence 11724, A	381	6	0.8	102	2	PCT-US96-10227-1	Sequence 1, Appl
309	6	0.8	69	2	US-09-732-210-1004	Sequence 1004, Ap	382	6	0.8	102	4	US-08-467-393-4	Sequence 4, Appl
310	6	0.8	70	1	US-08-691-814B-34	Sequence 34, Appl	383	6	0.8	103	1	US-08-209-747-4	Sequence 4, Appl
311	6	0.8	70	2	US-09-732-210-893	Sequence 893, App	384	6	0.8	103	1	US-08-458-298-4	Sequence 19, Appl
312	6	0.8	70	2	US-09-621-976-5508	Sequence 5508, App	385	6	0.8	103	1	US-08-710-749-19	Sequence 20, Appl
313	6	0.8	70	6	5453566-2	Patent No. 5453566	386	6	0.8	104	1	US-08-479-089A-5	Sequence 5, Appl
314	6	0.8	71	2	US-09-732-210-93	Sequence 93, Appl	387	6	0.8	104	2	US-08-710-749-20	Sequence 20, Appl
315	6	0.8	71	2	US-09-270-767-56690	Sequence 56690, A	388	6	0.8	104	2	US-08-479-089A-6	Sequence 6, Appl
316	6	0.8	71	2	US-09-949-016-8499	Sequence 8499, Ap	389	6	0.8	104	2	US-07-669-545B-5	Sequence 5, Appl
317	6	0.8	73	2	US-09-489-039A-12244	Sequence 12244, A	390	6	0.8	104	2	US-07-669-545B-6	Sequence 6, Appl
318	6	0.8	73	2	US-09-902-540-10252	Sequence 10252, A	391	6	0.8	104	2	US-09-147-875A-20	Sequence 20, Appl
319	6	0.8	74	2	US-09-543-681A-8341	Sequence 8341, Ap	392	6	0.8	104	2		

393	6	0.8	104	2	US-09-147-875A-21	Sequence 21, Appl	466	6	0.8	110	2	US-09-107-532A-6721	Sequence 6721, Ap
394	6	0.8	105	1	US-08-889-013C-6	Sequence 6, Appl	467	6	0.8	110	2	US-09-489-038A-10081	Sequence 10081, A
395	6	0.8	105	2	US-09-205-258-1082	Sequence 1082, Ap	468	6	0.8	110	2	US-09-902-540-11433	Sequence 11433, A
396	6	0.8	105	2	US-09-583-110-5144	Sequence 5144, Ap	469	6	0.8	112	2	US-09-543-681A-4827	Sequence 4827, Ap
397	6	0.8	105	2	US-09-640-211A-924	Sequence 924, App	470	6	0.8	112	2	US-09-710-279-2114	Sequence 2114, Ap
398	6	0.8	105	2	US-09-640-211A-2239	Sequence 2239, Ap	471	6	0.8	113	1	US-08-256-568B-85	Sequence 85, Appl
399	6	0.8	105	2	US-10-004-860-1082	Sequence 1082, Ap	472	6	0.8	113	2	US-09-038-369B-85	Sequence 85, Appl
400	6	0.8	106	1	US-07-732-242C-2	Sequence 2, Appl	473	6	0.8	113	2	US-08-836-075A-82	Sequence 82, Appl
401	6	0.8	106	1	US-08-290-592B-34	Sequence 34, Appl	474	6	0.8	113	2	US-08-836-075A-98	Sequence 98, Appl
402	6	0.8	106	1	US-08-290-592B-35	Sequence 35, Appl	475	6	0.8	113	2	US-09-378-900A-85	Sequence 85, Appl
403	6	0.8	106	1	US-08-956-047-33	Sequence 33, Appl	476	6	0.8	113	2	US-09-899-044-85	Sequence 85, Appl
404	6	0.8	106	2	US-08-397-411-8	Sequence 8, Appl	477	6	0.8	113	2	US-09-489-039A-8131	Sequence 8131, Ap
405	6	0.8	106	2	US-08-397-411-9	Sequence 9, Appl	478	6	0.8	113	2	US-09-878-281A-218	Sequence 218, App
406	6	0.8	106	2	US-09-771-415-1	Sequence 1, Appl	479	6	0.8	113	2	US-09-899-302-85	Sequence 85, Appl
407	6	0.8	106	2	US-09-771-415-17	Sequence 17, Appl	480	6	0.8	113	2	US-09-899-082B-85	Sequence 85, Appl
408	6	0.8	106	2	US-09-232-290-24	Sequence 24, Appl	481	6	0.8	113	2	US-09-899-082B-124	Sequence 124, App
409	6	0.8	106	2	US-09-996-288-8	Sequence 8, Appl	482	6	0.8	113	2	US-09-899-082B-125	Sequence 125, App
410	6	0.8	106	2	US-09-996-288-11	Sequence 11, Appl	483	6	0.8	114	2	US-09-710-279-2252	Sequence 2252, Ap
411	6	0.8	106	2	US-09-996-288-54	Sequence 54, Appl	484	6	0.8	114	2	US-09-513-999C-5777	Sequence 5777, Ap
412	6	0.8	106	2	US-09-996-265-8	Sequence 8, Appl	485	6	0.8	117	1	US-08-274-661B-38	Sequence 38, Appl
413	6	0.8	106	2	US-09-996-265-11	Sequence 11, Appl	486	6	0.8	117	2	US-09-513-999C-6175	Sequence 6175, Ap
414	6	0.8	106	2	PCT-US95-10053-31	Sequence 31, Appl	487	6	0.8	119	2	US-09-732-210-678	Sequence 678, App
415	6	0.8	106	4	PCT-US95-10053-32	Sequence 32, Appl	488	6	0.8	119	2	US-09-270-767-47348	Sequence 47348, A
416	6	0.8	106	4	PCT-US96-09448-34	Sequence 34, Appl	489	6	0.8	119	2	US-09-830-954A-28	Sequence 28, Appl
417	6	0.8	106	4	PCT-US96-09448-35	Sequence 35, Appl	490	6	0.8	120	2	US-09-308-345A-21	Sequence 21, Appl
418	6	0.8	106	4	PCT-US96-09448-35	Sequence 35, Appl	491	6	0.8	122	2	US-09-198-452A-510	Sequence 510, App
419	6	0.8	107	1	US-07-942-245-3	Sequence 3, Appl	492	6	0.8	122	2	US-09-270-767-33422	Sequence 33422, A
420	6	0.8	107	1	US-08-303-569B-25	Sequence 25, Appl	493	6	0.8	122	2	US-09-270-767-48639	Sequence 48639, A
421	6	0.8	107	1	US-08-303-569B-26	Sequence 26, Appl	494	6	0.8	122	2	US-09-902-540-13323	Sequence 13323, A
422	6	0.8	107	1	US-08-303-569B-27	Sequence 27, Appl	495	6	0.8	123	2	US-09-198-452A-625	Sequence 625, App
423	6	0.8	107	1	US-08-303-569B-28	Sequence 28, Appl	496	6	0.8	123	2	US-09-270-767-43402	Sequence 43402, A
424	6	0.8	107	1	US-08-303-569B-29	Sequence 29, Appl	497	6	0.8	123	2	US-09-438-185A-585	Sequence 585, App
425	6	0.8	107	1	US-08-070-116A-6	Sequence 6, Appl	498	6	0.8	124	2	US-09-509-738C-15	Sequence 15, Appl
426	6	0.8	107	1	US-08-070-116A-8	Sequence 8, Appl	499	6	0.8	126	1	US-08-656-586-6	Sequence 6, Appl
427	6	0.8	107	1	US-08-070-116A-9	Sequence 9, Appl	500	6	0.8	126	2	US-09-663-600A-102	Sequence 102, App
428	6	0.8	107	1	US-08-070-116A-18	Sequence 18, Appl	501	6	0.8	126	2	US-09-270-767-41467	Sequence 41467, A
429	6	0.8	107	1	US-08-116-247-8	Sequence 8, Appl	502	6	0.8	126	2	US-09-270-767-58058	Sequence 58058, A
430	6	0.8	107	1	US-08-116-247-26	Sequence 26, Appl	503	6	0.8	128	1	US-08-656-586-2	Sequence 2, Appl
431	6	0.8	107	1	US-08-116-247-27	Sequence 27, Appl	504	6	0.8	128	1	US-08-956-047-31	Sequence 31, Appl
432	6	0.8	107	1	US-08-116-247-28	Sequence 28, Appl	505	6	0.8	128	2	US-08-444-644-25	Sequence 25, Appl
433	6	0.8	107	1	US-08-116-247-29	Sequence 29, Appl	506	6	0.8	128	2	US-08-232-246A-25	Sequence 25, Appl
434	6	0.8	107	2	US-09-370-838-113	Sequence 113, App	507	6	0.8	128	2	US-09-134-001C-4164	Sequence 4164, Ap
435	6	0.8	107	2	US-08-557-050-6	Sequence 6, Appl	508	6	0.8	128	2	US-09-270-767-57599	Sequence 57599, A
436	6	0.8	107	2	US-08-557-050-8	Sequence 8, Appl	509	6	0.8	129	2	US-09-134-000C-5429	Sequence 5429, Ap
437	6	0.8	107	2	US-08-557-050-9	Sequence 9, Appl	510	6	0.8	129	2	US-09-513-999C-5540	Sequence 5540, Ap
438	6	0.8	107	2	US-09-795-515-25	Sequence 25, Appl	511	6	0.8	129	2	US-09-513-999C-8080	Sequence 8080, Ap
439	6	0.8	107	2	US-09-795-515-26	Sequence 26, Appl	512	6	0.8	129	2	US-09-902-540-12956	Sequence 12956, A
440	6	0.8	107	2	US-09-795-515-27	Sequence 27, Appl	513	6	0.8	131	2	US-09-270-767-38194	Sequence 38194, A
441	6	0.8	107	2	US-09-795-515-28	Sequence 28, Appl	514	6	0.8	131	2	US-09-270-767-53411	Sequence 53411, A
442	6	0.8	107	2	US-09-795-515-29	Sequence 29, Appl	515	6	0.8	133	2	US-09-621-976-6550	Sequence 6550, Ap
443	6	0.8	107	2	US-09-348-224-8	Sequence 8, Appl	516	6	0.8	134	2	US-08-529-055-65	Sequence 55, Appl
444	6	0.8	107	2	US-09-348-224-26	Sequence 26, Appl	517	6	0.8	134	2	US-09-248-796A-27186	Sequence 27186, A
445	6	0.8	107	2	US-09-348-224-27	Sequence 27, Appl	518	6	0.8	134	2	US-10-104-047-2098	Sequence 2098, Ap
446	6	0.8	107	2	US-09-348-224-28	Sequence 28, Appl	519	6	0.8	135	2	US-09-252-991A-22092	Sequence 22092, A
447	6	0.8	107	2	US-09-348-224-29	Sequence 29, Appl	520	6	0.8	135	2	US-09-107-433-5156	Sequence 5156, Ap
448	6	0.8	107	2	US-09-854-133B-113	Sequence 113, App	521	6	0.8	136	2	US-09-270-767-39814	Sequence 39814, A
449	6	0.8	107	4	PCT-US91-01360-3	Sequence 3, Appl	522	6	0.8	136	2	US-09-270-767-55031	Sequence 55031, A
450	6	0.8	108	1	US-08-710-749-24	Sequence 24, Appl	523	6	0.8	137	2	US-09-489-039A-7466	Sequence 7466, Ap
451	6	0.8	108	2	US-09-147-875A-25	Sequence 25, Appl	524	6	0.8	137	2	US-09-270-767-59938	Sequence 59938, A
452	6	0.8	108	2	US-09-726-219A-241	Sequence 241, App	525	6	0.8	138	2	US-09-472-087-79	Sequence 79, Appl
453	6	0.8	108	2	US-09-726-219A-242	Sequence 242, App	526	6	0.8	138	2	US-09-270-767-57429	Sequence 57429, A
454	6	0.8	108	2	US-09-726-219A-243	Sequence 243, App	527	6	0.8	139	2	US-09-252-991A-25939	Sequence 25939, A
455	6	0.8	108	2	US-09-726-219A-251	Sequence 251, App	528	6	0.8	139	2	US-09-902-540-10025	Sequence 10025, A
456	6	0.8	108	2	US-09-726-219A-252	Sequence 252, App	529	6	0.8	139	2	US-09-998-805-3	Sequence 3, Appl
457	6	0.8	108	2	US-09-726-219A-253	Sequence 253, App	530	6	0.8	140	2	US-09-248-796A-27587	Sequence 27587, A
458	6	0.8	108	2	US-09-196-522-241	Sequence 241, App	531	6	0.8	141	2	US-09-286-981B-2	Sequence 2, Appl
459	6	0.8	108	2	US-09-196-522-242	Sequence 242, App	532	6	0.8	141	2	US-09-270-767-43497	Sequence 43497, A
460	6	0.8	108	2	US-09-196-522-243	Sequence 243, App	533	6	0.8	141	2	US-10-254-995-2	Sequence 2, Appl
461	6	0.8	108	2	US-09-196-522-251	Sequence 251, App	534	6	0.8	142	2	US-09-252-991A-27627	Sequence 27627, A
462	6	0.8	108	2	US-09-196-522-252	Sequence 252, App	535	6	0.8	143	2	US-09-039-859-7	Sequence 7, Appl
463	6	0.8	108	2	US-09-196-522-253	Sequence 253, App	536	6	0.8	143	2	US-09-252-991A-22066	Sequence 22066, A
464	6	0.8	110	2	US-08-836-561-33	Sequence 33, Appl	537	6	0.8	143	2	US-09-252-991A-29827	Sequence 29827, A
465	6	0.8	110	2	US-08-434-122-33	Sequence 33, Appl	538	6	0.8	144	1	US-08-133-979A-21	Sequence 21, Appl

539	6	0.8	144	1	US-08-436-890-21	Sequence 21, Appl	612	169	2	US-09-248-796A-26743	Sequence 26743, A
540	6	0.8	144	1	US-08-451-213-21	Sequence 21, Appl	613	170	2	US-09-732-210-558	Sequence 558, App
541	6	0.8	144	2	US-10-104-047-3457	Sequence 3457, App	614	170	2	US-08-529-055-60	Sequence 60, Appl
542	6	0.8	145	2	US-09-602-787A-330	Sequence 330, App	615	171	2	US-09-248-796A-27723	Sequence 27723, A
543	6	0.8	145	2	US-09-640-211A-698	Sequence 698, App	616	172	2	US-09-583-110-3305	Sequence 3305, Ap
544	6	0.8	145	2	US-09-902-540-13747	Sequence 13747, A	617	173	2	US-09-270-767-32051	Sequence 32051, A
545	6	0.8	146	2	US-09-252-91A-24703	Sequence 24703, A	618	173	2	US-09-270-767-47268	Sequence 47268, A
546	6	0.8	146	2	US-09-902-540-13495	Sequence 13495, A	619	174	2	US-09-149-476-413	Sequence 413, App
547	6	0.8	147	2	US-09-602-787A-332	Sequence 332, App	620	174	2	US-09-270-767-40521	Sequence 40521, A
548	6	0.8	148	2	US-09-328-352-8000	Sequence 8000, App	621	175	2	US-09-270-767-55737	Sequence 55737, A
549	6	0.8	150	2	US-08-857-076-17	Sequence 17, Appl	622	175	2	US-09-252-991A-28806	Sequence 28806, A
550	6	0.8	150	2	US-09-663-600A-196	Sequence 196, App	623	176	2	US-09-780-717-2	Sequence 2, Appl
551	6	0.8	150	2	US-09-205-658-17	Sequence 17, Appl	624	176	2	US-09-248-796A-20163	Sequence 20163, A
552	6	0.8	151	2	US-09-252-991A-16814	Sequence 16814, A	625	176	2	US-09-248-796A-25947	Sequence 25947, A
553	6	0.8	151	2	US-09-328-352-5751	Sequence 5751, App	626	177	2	US-09-248-796A-24917	Sequence 24917, A
554	6	0.8	151	2	US-09-540-236-2801	Sequence 2801, A	627	178	2	US-08-671-548C-14	Sequence 14, Appl
555	6	0.8	151	2	US-09-248-796A-16825	Sequence 16825, A	628	178	2	US-09-732-210-1077	Sequence 1077, Ap
556	6	0.8	152	2	US-09-270-767-48811	Sequence 48811, A	629	180	2	US-08-284-667A-14	Sequence 14, Appl
557	6	0.8	153	2	US-09-732-210-1748	Sequence 1748, App	630	180	2	US-09-252-991A-17913	Sequence 17913, A
558	6	0.8	153	2	US-09-270-767-32681	Sequence 32681, A	631	181	2	US-08-529-055-42	Sequence 42, Appl
559	6	0.8	153	2	US-09-270-767-47898	Sequence 47898, A	632	182	1	US-08-529-055-42	Sequence 93, Appl
560	6	0.8	153	2	US-09-902-540-12086	Sequence 12086, A	633	182	2	US-08-529-055-50	Sequence 50, Appl
561	6	0.8	155	1	US-08-209-747-15	Sequence 15, Appl	634	183	2	US-09-122-443-13	Sequence 13, Appl
562	6	0.8	155	1	US-08-458-298-15	Sequence 15, Appl	635	184	2	US-09-558-087-13	Sequence 13, Appl
563	6	0.8	155	2	US-09-489-039A-7828	Sequence 7828, App	636	184	2	US-09-558-087-13	Sequence 13, Appl
564	6	0.8	156	2	US-09-134-000C-6299	Sequence 6299, App	637	184	2	US-09-558-087-13	Sequence 13, Appl
565	6	0.8	157	2	US-09-328-352-4165	Sequence 4165, App	638	184	2	US-09-558-087-13	Sequence 13, Appl
566	6	0.8	157	2	US-09-902-540-14881	Sequence 14881, A	639	184	2	US-09-558-087-13	Sequence 13, Appl
567	6	0.8	158	2	US-09-252-991A-29352	Sequence 29352, A	640	185	2	US-08-529-055-46	Sequence 46, Appl
568	6	0.8	158	2	US-09-134-000C-4025	Sequence 4025, App	641	186	2	US-09-902-540-14912	Sequence 14912, A
569	6	0.8	158	2	US-09-265-585C-130	Sequence 130, App	642	187	2	US-09-270-767-45734	Sequence 45734, A
570	6	0.8	159	2	US-09-252-991A-22914	Sequence 22914, A	643	187	2	US-09-248-796A-19329	Sequence 19329, A
571	6	0.8	159	2	US-09-602-787A-102	Sequence 102, App	644	188	2	US-08-529-055-59	Sequence 59, Appl
572	6	0.8	159	2	US-09-270-767-37981	Sequence 37981, A	645	188	2	US-09-489-039A-13533	Sequence 13533, A
573	6	0.8	159	2	US-09-270-767-46525	Sequence 46525, A	646	188	2	US-09-902-540-12348	Sequence 12348, A
574	6	0.8	159	2	US-09-270-767-53198	Sequence 53198, A	647	189	2	US-09-252-991A-30049	Sequence 30049, A
575	6	0.8	160	2	US-09-117-257-38	Sequence 38, Appl	648	191	2	US-08-671-548C-2	Sequence 2, Appl
576	6	0.8	160	2	US-09-489-352-38	Sequence 38, Appl	649	191	2	US-09-252-991A-24515	Sequence 24515, A
577	6	0.8	160	2	US-08-858-207A-322	Sequence 322, App	650	191	2	US-09-328-352-6761	Sequence 6761, A
578	6	0.8	160	2	US-09-252-991A-16641	Sequence 16641, A	651	191	2	US-09-640-211A-1080	Sequence 1080, Ap
579	6	0.8	160	2	US-09-621-976-6030	Sequence 6030, App	652	192	2	US-08-284-667A-2	Sequence 2, Appl
580	6	0.8	160	2	US-09-270-767-39354	Sequence 39354, A	653	192	2	US-09-149-476-419	Sequence 419, App
581	6	0.8	160	2	US-09-270-767-45565	Sequence 45565, A	654	192	2	US-09-543-681A-7846	Sequence 7846, Ap
582	6	0.8	160	2	US-09-270-767-54571	Sequence 54571, A	655	193	2	US-08-671-548C-16	Sequence 16, Appl
583	6	0.8	161	2	US-09-902-540-10892	Sequence 10892, A	656	193	2	US-08-284-667A-16	Sequence 16, Appl
584	6	0.8	161	2	US-09-902-540-16115	Sequence 16115, A	657	194	2	US-08-248-796A-27860	Sequence 27860, A
585	6	0.8	162	2	US-09-446-504-27	Sequence 27, Appl	658	195	1	US-08-403-852D-24	Sequence 24, Appl
586	6	0.8	162	2	US-09-712-266-27	Sequence 27, Appl	659	195	2	US-08-510-646B-25	Sequence 25, Appl
587	6	0.8	162	2	US-09-499-148-5	Sequence 5, Appl	660	195	2	US-09-231-818-24	Sequence 24, Appl
588	6	0.8	162	2	US-09-270-767-43246	Sequence 43246, A	661	195	2	US-09-583-110-4558	Sequence 4558, Ap
589	6	0.8	164	2	US-09-270-767-33348	Sequence 33348, A	662	196	2	US-09-635-359B-24	Sequence 379, App
590	6	0.8	164	2	US-09-270-767-48565	Sequence 48565, A	663	196	2	US-09-711-164-379	Sequence 7659, Ap
591	6	0.8	165	2	US-09-513-999C-7900	Sequence 7900, App	664	197	1	US-08-567-509-1	Sequence 1, Appl
592	6	0.8	166	2	US-09-252-991A-19472	Sequence 19472, A	665	197	1	US-08-779-870-1	Sequence 44, Appl
593	6	0.8	166	2	US-09-889-463A-12	Sequence 12, Appl	666	198	2	US-08-529-055-44	Sequence 44, Appl
594	6	0.8	167	2	US-09-062-440-8	Sequence 8, Appl	667	198	2	US-08-523-055-36	Sequence 36, Appl
595	6	0.8	167	2	US-09-062-440-9	Sequence 9, Appl	668	198	2	US-08-523-055-61	Sequence 61, Appl
596	6	0.8	167	2	US-09-062-440-11	Sequence 11, Appl	669	198	2	US-09-270-767-36571	Sequence 36571, A
597	6	0.8	167	2	US-09-712-495-8	Sequence 8, Appl	670	198	2	US-09-270-767-44202	Sequence 44202, A
598	6	0.8	167	2	US-09-712-495-9	Sequence 9, Appl	671	198	2	US-09-270-767-51788	Sequence 51788, A
599	6	0.8	167	2	US-09-712-495-11	Sequence 11, Appl	672	198	2	US-09-538-092-1045	Sequence 1045, Ap
600	6	0.8	167	2	US-09-252-991A-31970	Sequence 31970, A	673	198	2	US-09-949-016-7318	Sequence 7318, Ap
601	6	0.8	167	2	US-09-902-540-14730	Sequence 14730, A	674	200	2	US-09-270-767-32508	Sequence 32508, A
602	6	0.8	168	2	US-08-679-006-30	Sequence 30, Appl	675	200	2	US-09-270-767-47725	Sequence 47725, A
603	6	0.8	168	2	US-09-107-532A-3745	Sequence 3745, App	676	201	2	US-09-270-767-32368	Sequence 32368, A
604	6	0.8	168	2	US-09-134-000C-4552	Sequence 4552, App	677	201	2	US-09-270-767-47585	Sequence 47585, A
605	6	0.8	168	2	US-09-398-405-30	Sequence 30, Appl	678	202	2	US-09-949-016-7318	Sequence 7318, Ap
606	6	0.8	168	2	US-09-252-991A-31389	Sequence 31389, A	679	203	2	US-09-134-001C-3696	Sequence 3696, Ap
607	6	0.8	169	2	US-09-270-767-36359	Sequence 36359, A	680	203	2	US-09-248-796A-20648	Sequence 20648, A
608	6	0.8	169	2	US-09-270-767-39082	Sequence 39082, A	681	203	2	US-09-605-703B-1122	Sequence 1122, Ap
609	6	0.8	169	2	US-09-270-767-51576	Sequence 51576, A	682	203	2	US-09-605-703B-1124	Sequence 1124, Ap
610	6	0.8	169	2	US-09-270-767-51576	Sequence 51576, A	683	204	2	US-09-328-352-6644	Sequence 6644, Ap
611	6	0.8	169	2	US-09-270-767-54299	Sequence 54299, A	684				

685	6	0.8	204	2	US-08-529-055-51	Sequence 51, Appl	758	234	2	US-08-836-236-4	Sequence 4, Appl
686	6	0.8	204	2	US-08-529-055-58	Sequence 58, Appl	759	234	2	US-08-836-236-5	Sequence 5, Appl
687	6	0.8	204	2	US-09-710-279-2394	Sequence 2394, Ap	760	234	2	US-08-715-628B-3	Sequence 3, Appl
688	6	0.8	205	2	US-09-710-279-3020	Sequence 3020, Ap	761	234	2	US-09-535-679-4	Sequence 4, Appl
689	6	0.8	206	2	US-09-134-001C-4621	Sequence 4621, Ap	762	234	2	US-09-535-679-5	Sequence 5, Appl
690	6	0.8	206	2	US-08-529-055-54	Sequence 54, Appl	763	235	1	US-08-190-199A-61	Sequence 61, Appl
691	6	0.8	207	2	US-09-046-894-33	Sequence 33, Appl	764	235	1	US-08-303-569B-5	Sequence 5, Appl
692	6	0.8	208	2	US-09-134-001C-4132	Sequence 4132, Ap	765	235	1	US-08-116-247-5	Sequence 5, Appl
693	6	0.8	209	2	US-09-583-110-2988	Sequence 2988, Ap	766	235	2	US-09-795-515-5	Sequence 5, Appl
694	6	0.8	209	2	US-09-107-433-3989	Sequence 3989, Ap	767	235	2	US-09-270-767-48485	Sequence 48485, A
695	6	0.8	209	2	US-10-135-636-11	Sequence 11, Appl	768	235	2	US-09-248-796A-18489	Sequence 18489, A
696	6	0.8	210	2	US-09-543-681A-7093	Sequence 7093, Ap	769	235	2	US-09-348-224-5	Sequence 5, Appl
697	6	0.8	211	2	US-09-902-540-10681	Sequence 10681, A	770	235	2	US-09-949-016-7903	Sequence 7903, Ap
698	6	0.8	212	2	US-09-543-681A-6089	Sequence 6089, Ap	771	236	1	US-08-190-199A-65	Sequence 65, Appl
699	6	0.8	212	2	US-09-248-796A-15317	Sequence 15317, A	772	236	2	US-08-411-768B-8	Sequence 8, Appl
700	6	0.8	213	1	US-08-941-263-3	Sequence 3, Appl	773	236	2	US-09-543-681A-6359	Sequence 6359, Ap
701	6	0.8	213	2	US-09-227-178-3	Sequence 12, Appl	774	236	2	US-09-827-688-2	Sequence 2, Appl
702	6	0.8	213	2	US-08-397-411-12	Sequence 12, Appl	775	237	2	US-09-320-878-11	Sequence 11, Appl
703	6	0.8	213	2	US-09-470-449-3	Sequence 3, Appl	776	237	2	US-09-105-537-18	Sequence 18, Appl
704	6	0.8	213	2	US-08-726-775-3	Sequence 3, Appl	777	237	2	US-09-216-295-19	Sequence 19, Appl
705	6	0.8	213	2	US-09-252-991A-25866	Sequence 25866, A	778	237	2	US-09-657-440-11	Sequence 11, Appl
706	6	0.8	213	2	US-08-529-055-47	Sequence 47, Appl	779	237	2	US-09-252-991A-19656	Sequence 19656, A
707	6	0.8	213	2	US-09-996-288-209	Sequence 209, App	780	237	2	US-09-543-681A-5471	Sequence 5471, Ap
708	6	0.8	213	2	US-09-996-288-231	Sequence 231, App	781	237	2	US-09-632-570-19	Sequence 19, Appl
709	6	0.8	213	2	US-09-996-288-255	Sequence 255, App	782	237	2	US-09-632-575-49	Sequence 49, Appl
710	6	0.8	213	2	US-09-603-208A-124	Sequence 124, App	783	237	2	US-09-793-708-11	Sequence 11, Appl
711	6	0.8	213	2	US-09-902-540-13705	Sequence 13705, A	784	238	2	US-09-328-352-6703	Sequence 6703, Ap
712	6	0.8	213	2	US-09-996-265-209	Sequence 209, App	785	238	2	US-09-543-681A-4429	Sequence 4429, Ap
713	6	0.8	213	2	US-09-996-265-231	Sequence 231, App	786	239	2	US-09-540-236-3366	Sequence 3366, Ap
714	6	0.8	213	2	US-09-996-265-255	Sequence 255, App	787	239	2	US-09-248-796A-15852	Sequence 15852, A
715	6	0.8	213	2	US-10-135-636-7	Sequence 7, Appl	788	239	2	US-09-107-433-3281	Sequence 3281, Ap
716	6	0.8	214	2	US-09-543-681A-6408	Sequence 6408, Ap	789	239	2	US-09-830-954B-6	Sequence 6, Appl
717	6	0.8	214	2	US-09-270-767-42972	Sequence 42972, A	790	240	1	US-08-356-047-25	Sequence 25, Appl
718	6	0.8	214	2	US-09-893-737-306	Sequence 306, App	791	240	2	US-09-540-236-2994	Sequence 2994, Ap
719	6	0.8	215	2	US-09-252-991A-22038	Sequence 22038, A	792	240	2	US-09-270-767-48132	Sequence 48132, A
720	6	0.8	216	2	US-09-543-681A-6821	Sequence 6821, Ap	793	241	2	US-09-370-838-194	Sequence 194, App
721	6	0.8	216	2	US-09-071-035-312	Sequence 312, App	794	241	2	US-09-387-372-4	Sequence 4, Appl
722	6	0.8	217	2	US-09-484-577A-30	Sequence 30, Appl	795	241	2	US-09-270-767-38616	Sequence 38616, A
723	6	0.8	217	2	US-09-391-606-7	Sequence 7, Appl	796	241	2	US-09-270-767-40378	Sequence 40378, A
724	6	0.8	217	2	US-10-206-576-312	Sequence 312, App	797	241	2	US-09-270-767-53833	Sequence 53833, A
725	6	0.8	218	2	US-09-270-767-43455	Sequence 43455, A	798	241	2	US-09-270-767-55794	Sequence 55794, A
726	6	0.8	218	2	US-09-248-796A-16056	Sequence 16056, A	799	241	2	US-09-854-133-194	Sequence 194, App
727	6	0.8	218	2	US-09-107-433-3578	Sequence 3578, Ap	800	241	2	US-09-581-345-5	Sequence 5, Appl
728	6	0.8	218	2	US-09-902-540-13913	Sequence 13913, A	801	241	2	US-09-902-540-9790	Sequence 9790, Ap
729	6	0.8	219	1	US-08-401-068-6	Sequence 6, Appl	802	241	2	US-09-774-490-4	Sequence 4, Appl
730	6	0.8	219	1	US-08-846-338-6	Sequence 6, Appl	803	242	2	US-09-583-110-3522	Sequence 3522, Ap
731	6	0.8	219	2	US-09-198-452A-634	Sequence 634, App	804	242	2	US-09-959-392-34	Sequence 34, Appl
732	6	0.8	219	2	US-09-438-185A-593	Sequence 593, App	805	242	2	US-09-949-016-10911	Sequence 10911, A
733	6	0.8	220	2	US-09-853-450-38	Sequence 38, Appl	806	245	2	US-09-071-035-310	Sequence 310, App
734	6	0.8	221	2	US-09-198-452A-292	Sequence 292, App	807	245	2	US-10-206-576-310	Sequence 310, App
735	6	0.8	222	1	US-09-190-199A-67	Sequence 67, Appl	808	246	2	US-09-336-536-31	Sequence 31, Appl
736	6	0.8	222	2	US-09-252-991A-21377	Sequence 21377, A	809	246	2	US-09-134-000C-5137	Sequence 5137, Ap
737	6	0.8	223	1	US-09-190-199A-63	Sequence 63, Appl	810	246	2	US-09-244-805-32	Sequence 32, Appl
738	6	0.8	223	2	US-09-252-991A-17072	Sequence 17072, A	811	248	2	US-09-248-796A-18654	Sequence 18654, A
739	6	0.8	224	2	US-09-489-039A-1321	Sequence 13921, A	812	248	2	US-09-248-796A-18980	Sequence 18980, A
740	6	0.8	224	2	US-09-248-796A-18609	Sequence 18609, A	813	248	2	US-10-144-198-33	Sequence 33, Appl
741	6	0.8	224	2	US-09-438-185A-281	Sequence 281, App	814	248	2	US-09-502-540-11644	Sequence 11644, A
742	6	0.8	225	2	US-09-270-767-47945	Sequence 47945, A	815	248	2	US-10-012-231A-194	Sequence 194, App
743	6	0.8	225	2	US-09-270-767-47945	Sequence 47945, A	816	248	2	US-10-015-389A-194	Sequence 194, App
744	6	0.8	225	2	US-09-710-279-1594	Sequence 1594, Ap	817	248	2	US-10-006-768A-194	Sequence 194, App
745	6	0.8	226	2	US-09-252-991A-17294	Sequence 17294, A	818	248	2	US-10-015-671A-194	Sequence 194, App
746	6	0.8	226	2	US-09-270-767-60023	Sequence 60023, A	819	248	2	US-10-015-393A-194	Sequence 194, App
747	6	0.8	227	2	US-09-252-991A-30027	Sequence 30027, A	820	248	2	US-10-011-833A-194	Sequence 194, App
748	6	0.8	229	2	US-09-107-532A-6064	Sequence 6064, Ap	821	248	2	US-10-006-041A-194	Sequence 194, App
749	6	0.8	231	2	US-10-112-802-1	Sequence 1, Appl	822	248	2	US-10-012-064A-194	Sequence 194, App
750	6	0.8	231	2	US-09-270-767-43196	Sequence 43196, A	823	249	1	US-08-685-992-8	Sequence 8, Appl
751	6	0.8	232	2	US-08-529-055-70	Sequence 70, Appl	824	249	1	US-09-144-925-8	Sequence 8, Appl
752	6	0.8	232	2	US-09-248-796A-14122	Sequence 14122, A	825	249	2	US-09-949-016-8151	Sequence 8151, Ap
753	6	0.8	233	2	US-09-252-991A-20802	Sequence 20802, A	826	250	2	US-09-489-039A-9843	Sequence 9843, Ap
754	6	0.8	233	2	US-09-252-991A-21274	Sequence 21274, A	827	250	2	US-09-134-000C-4602	Sequence 4602, Ap
755	6	0.8	233	2	US-09-252-991A-21316	Sequence 21316, A	828	251	1	US-08-209-747-8	Sequence 8, Appl
756	6	0.8	233	2	US-09-270-767-43719	Sequence 43719, A	829	251	1	US-08-458-298-8	Sequence 8, Appl
757	6	0.8	233	2	US-09-605-703B-2388	Sequence 2388, Ap	830	251	2	US-09-902-540-15293	Sequence 15293, A



831	6	0.8	252	2	US-09-252-991A-16901	Sequence 16901, A	904	0.8	276	2	US-09-765-271-134	Sequence 134, App
832	6	0.8	252	2	US-09-583-110-3303	Sequence 3303, Ap	905	0.8	276	2	US-09-765-272A-134	Sequence 134, App
833	6	0.8	252	2	US-09-270-767-47090	Sequence 47090, A	906	0.8	279	2	US-09-314-701-60	Sequence 60, Appl
834	6	0.8	253	2	US-09-336-910A-7	Sequence 7, Appl	907	0.8	279	2	US-09-543-681A-4433	Sequence 4433, Ap
835	6	0.8	253	2	US-09-902-540-14305	Sequence 14305, A	908	0.8	279	2	US-09-270-767-33415	Sequence 33415, A
836	6	0.8	254	2	US-09-252-991A-22771	Sequence 22771, A	909	0.8	279	2	US-09-270-767-48632	Sequence 48632, A
837	6	0.8	254	2	US-09-134-000C-4199	Sequence 4199, Ap	910	0.8	279	2	US-10-144-198-10	Sequence 10, Appl
838	6	0.8	254	2	US-09-586-106D-159	Sequence 159, App	911	0.8	279	2	US-10-314-639-60	Sequence 60, Appl
839	6	0.8	254	2	US-09-949-016-6948	Sequence 6948, Ap	912	0.8	279	2	US-10-059-964A-60	Sequence 7715, Ap
840	6	0.8	254	2	US-10-799-870-159	Sequence 870, Ap	913	0.8	280	2	US-09-489-039A-7715	Sequence 4231, Ap
841	6	0.8	255	2	US-09-553-498-8	Sequence 8, Appl	914	0.8	280	2	US-10-159-901-49	Sequence 43, Appl
842	6	0.8	255	2	US-09-618-869-8	Sequence 3420, Ap	915	0.8	280	2	US-09-252-991A-29199	Sequence 29199, A
843	6	0.8	255	2	US-09-540-236-3420	Sequence 3420, Ap	916	0.8	281	2	US-09-248-796A-14445	Sequence 14445, A
844	6	0.8	255	2	US-09-902-540-16637	Sequence 16637, A	917	0.8	282	2	US-09-270-767-45300	Sequence 45300, A
845	6	0.8	255	2	US-09-292-412-2	Sequence 2, Appl	918	0.8	282	2	US-08-592-214A-24	Sequence 24, Appl
846	6	0.8	256	2	US-09-089-019-12	Sequence 12, Appl	919	0.8	284	1	US-08-559-188-20	Sequence 20, Appl
847	6	0.8	256	2	US-09-252-991A-32307	Sequence 32307, A	920	0.8	284	2	US-08-655-227-20	Sequence 20, Appl
848	6	0.8	256	2	US-09-107-532A-3657	Sequence 3657, Ap	921	0.8	284	2	US-08-655-241-20	Sequence 20, Appl
849	6	0.8	256	2	US-09-583-110-4113	Sequence 4113, Ap	922	0.8	284	2	US-09-149-976-24	Sequence 24, Appl
850	6	0.8	256	2	US-10-138-701-6	Sequence 6, Appl	923	0.8	284	2	US-09-398-326-20	Sequence 20, Appl
851	6	0.8	256	2	US-09-292-411A-2	Sequence 2, Appl	924	0.8	284	2	US-09-134-000C-5638	Sequence 5638, Ap
852	6	0.8	257	2	US-09-902-540-12724	Sequence 12724, A	925	0.8	284	2	US-09-853-450-20	Sequence 20, Appl
853	6	0.8	257	2	US-09-328-352-4324	Sequence 4324, Ap	926	0.8	285	2	US-09-540-236-2157	Sequence 2157, Ap
854	6	0.8	258	2	US-09-724-623-105	Sequence 105, App	927	0.8	285	2	US-08-312-949-4	Sequence 4, Appl
855	6	0.8	258	2	US-09-023-942A-8	Sequence 8, Appl	928	0.8	288	2	US-08-446-201-4	Sequence 4, Appl
856	6	0.8	258	2	US-09-081-385-150	Sequence 150, App	929	0.8	288	2	US-09-252-991A-20608	Sequence 20608, A
857	6	0.8	258	2	US-09-270-767-32398	Sequence 32398, A	930	0.8	288	2	US-09-949-016-10862	Sequence 10862, A
858	6	0.8	258	2	US-09-270-767-43894	Sequence 43894, A	931	0.8	288	1	US-08-072-070-4	Sequence 4, Appl
859	6	0.8	258	2	US-09-270-767-59125	Sequence 59125, A	932	0.8	288	1	US-08-469-434-4	Sequence 4, Appl
860	6	0.8	258	2	US-09-752-639-150	Sequence 150, App	933	0.8	289	1	US-08-214-222-4	Sequence 4, Appl
861	6	0.8	258	2	US-09-712-813-150	Sequence 150, App	934	0.8	289	1	US-08-467-852A-5	Sequence 5, Appl
862	6	0.8	258	2	US-09-700-354A-150	Sequence 150, App	935	0.8	289	1	US-08-468-718-4	Sequence 4, Appl
863	6	0.8	258	2	US-09-605-703B-450	Sequence 450, App	936	0.8	289	1	US-08-247-431A-5	Sequence 5, Appl
864	6	0.8	258	2	US-09-605-703B-452	Sequence 452, App	937	0.8	289	1	US-09-543-681A-8235	Sequence 8235, Ap
865	6	0.8	259	2	US-09-270-767-45089	Sequence 45089, A	938	0.8	289	2	US-09-583-110-3563	Sequence 3563, Ap
866	6	0.8	259	2	US-10-320-104B-2	Sequence 2, Appl	939	0.8	289	2	US-09-134-001C-4918	Sequence 4918, Ap
867	6	0.8	260	2	US-09-134-001C-4009	Sequence 4009, Ap	940	0.8	290	2	US-09-107-532A-3841	Sequence 3841, Ap
868	6	0.8	260	2	US-09-489-039A-7421	Sequence 7421, Ap	941	0.8	290	2	US-09-743-847-2	Sequence 2, Appl
869	6	0.8	260	2	US-09-270-767-33511	Sequence 33511, A	942	0.8	290	2	US-09-248-796A-18749	Sequence 18749, A
870	6	0.8	260	2	US-09-270-767-46440	Sequence 46440, A	943	0.8	290	2	US-09-134-000C-4458	Sequence 4458, Ap
871	6	0.8	260	2	US-09-248-796A-17592	Sequence 17592, A	944	0.8	291	2	US-09-634-238-236	Sequence 236, App
872	6	0.8	261	2	US-09-489-039A-10725	Sequence 10725, A	945	0.8	292	2	US-09-270-767-43846	Sequence 43846, A
873	6	0.8	263	2	US-09-252-991A-23754	Sequence 23754, A	946	0.8	292	2	US-09-107-433-4868	Sequence 4868, Ap
874	6	0.8	264	2	US-09-035-382-4	Sequence 4, Appl	947	0.8	292	2	US-09-252-991A-27745	Sequence 27745, A
875	6	0.8	264	2	US-09-252-991A-27675	Sequence 27675, A	948	0.8	293	2	US-09-949-016-8027	Sequence 8027, Ap
876	6	0.8	264	2	US-09-134-000C-4403	Sequence 4403, Ap	949	0.8	293	2	US-09-252-991A-26450	Sequence 26450, A
877	6	0.8	264	2	US-09-902-540-16652	Sequence 16652, A	950	0.8	294	2	US-09-252-991A-268	Sequence 268, App
878	6	0.8	265	2	US-10-104-047-2141	Sequence 2141, Ap	951	0.8	295	2	US-09-198-452A-268	Sequence 45025, A
879	6	0.8	266	2	US-09-050-739-133	Sequence 153, App	952	0.8	295	2	US-09-270-767-45025	Sequence 45025, A
880	6	0.8	266	2	US-09-655-908-20	Sequence 20, Appl	953	0.8	295	2	US-09-438-185A-258	Sequence 42478, A
881	6	0.8	266	2	US-09-248-796A-20084	Sequence 20084, A	954	0.8	295	2	US-09-270-767-42478	Sequence 48808, A
882	6	0.8	266	2	US-09-902-540-13043	Sequence 13043, A	955	0.8	296	2	US-09-314-701-14	Sequence 14, Appl
883	6	0.8	267	2	US-09-489-039A-13450	Sequence 13450, A	956	0.8	297	2	US-09-489-039A-10089	Sequence 10089, A
884	6	0.8	267	2	US-09-976-594-212	Sequence 212, App	957	0.8	297	2	US-10-314-639-14	Sequence 14, Appl
885	6	0.8	267	2	US-09-248-796A-18561	Sequence 18561, A	958	0.8	297	2	US-10-059-964A-14	Sequence 14, Appl
886	6	0.8	267	2	US-09-902-540-14651	Sequence 14651, A	959	0.8	297	2	US-09-543-681A-6110	Sequence 6110, Ap
887	6	0.8	268	2	US-09-328-352-8118	Sequence 8118, Ap	960	0.8	298	2	US-09-248-796A-27737	Sequence 27737, A
888	6	0.8	269	2	US-09-540-236-3336	Sequence 3336, Ap	961	0.8	298	2	US-09-270-767-42307	Sequence 42307, A
889	6	0.8	269	2	US-09-583-110-3865	Sequence 3865, Ap	962	0.8	299	2	US-09-710-279-1192	Sequence 1192, Ap
890	6	0.8	269	2	US-09-270-767-42664	Sequence 42664, A	963	0.8	299	2	US-09-710-279-1768	Sequence 1768, Ap
891	6	0.8	270	2	US-08-878-474-1	Sequence 1, Appl	964	0.8	299	2	US-09-270-767-44496	Sequence 44496, A
892	6	0.8	270	2	US-09-107-433-5194	Sequence 5194, Ap	965	0.8	300	2	US-09-489-039A-10251	Sequence 10251, A
893	6	0.8	271	2	US-09-540-236-2326	Sequence 2326, Ap	966	0.8	301	2	US-09-902-540-12303	Sequence 12303, A
894	6	0.8	271	2	US-09-270-767-46455	Sequence 46455, A	967	0.8	301	2	US-08-303-861-20	Sequence 20, Appl
895	6	0.8	271	6	5175255-1	Patent No. 5175255	968	0.8	302	2	US-09-457-046B-24	Sequence 24, Appl
896	6	0.8	272	2	US-09-902-540-16810	Sequence 16810, A	969	0.8	302	2	US-09-252-991A-22159	Sequence 22159, A
897	6	0.8	273	2	US-09-252-991A-25600	Sequence 25600, A	970	0.8	302	2	US-09-107-532A-6924	Sequence 6924, Ap
898	6	0.8	274	2	US-09-489-039A-14339	Sequence 14339, A	971	0.8	302	2	US-09-866-570B-24	Sequence 24, Appl
899	6	0.8	274	2	US-10-104-047-3353	Sequence 3353, Ap	972	0.8	302	2	US-09-248-796A-15374	Sequence 15374, A
900	6	0.8	276	2	US-08-961-083-134	Sequence 134, App	973	0.8	302	2	US-09-248-796A-15270	Sequence 15270, A
901	6	0.8	276	2	US-09-252-991A-17951	Sequence 17951, A	974	0.8	303	2		
902	6	0.8	276	2	US-09-536-784-134	Sequence 134, App	975	0.8	304	2		
903	6	0.8	276	2	US-09-902-540-15737	Sequence 15737, A	976	0.8				

```

977 6 0.8 304 2 US-09-902-540-14051 Sequence 14051, A
978 6 0.8 305 2 US-09-248-796A-17837 Sequence 17837, A
979 6 0.8 305 2 US-09-248-796A-24107 Sequence 24107, A
980 6 0.8 305 2 US-09-949-016-7706 Sequence 7706, Ap
981 6 0.8 306 2 US-09-489-039A-10306 Sequence 10306, A
982 6 0.8 306 2 US-09-107-433-2663 Sequence 2663, Ap
983 6 0.8 307 2 US-09-134-001C-3792 Sequence 3792, Ap
984 6 0.8 307 2 US-09-270-767-44911 Sequence 44911, A
985 6 0.8 308 2 US-09-252-991A-27249 Sequence 27249, A
986 6 0.8 308 2 US-09-328-352-6762 Sequence 6762, Ap
987 6 0.8 309 2 US-09-270-767-44995 Sequence 44995, A
988 6 0.8 309 2 US-10-759-889-2 Sequence 2, Appl1
989 6 0.8 310 2 US-09-543-681A-6858 Sequence 6858, Ap
990 6 0.8 310 2 US-09-538-092-690 Sequence 690, App
991 6 0.8 311 2 US-09-107-532A-4438 Sequence 4438, Ap
992 6 0.8 311 2 US-09-107-532A-4439 Sequence 4439, Ap
993 6 0.8 312 2 US-09-107-433-2823 Sequence 2823, Ap
994 6 0.8 312 2 US-09-538-092-42 Sequence 42, Appl1
995 6 0.8 313 2 US-09-387-574-4 Sequence 4, Appl1
996 6 0.8 313 2 US-09-396-651B-3 Sequence 3, Appl1
997 6 0.8 313 2 US-09-668-096-4 Sequence 4, Appl1
998 6 0.8 313 2 US-09-470-512A-2 Sequence 2, Appl1
999 6 0.8 313 2 US-09-470-512A-10 Sequence 10, Appl1
1000 6 0.8 313 2 US-09-543-681A-8278 Sequence 8278, Ap

ALIGNMENTS

RESULT 1
US-09-994-192-4
; Sequence 4, Application US/09994192
; Patent No. 6610306
; GENERAL INFORMATION:
; APPLICANT: Judd, Ralph C.
; APPLICANT: Manning, Scott D.
; TITLE OF INVENTION: Omp85 Proteins of Neisseria gonorrhoeae and Neisseria meningitidis
; FILE REFERENCE: USBC147AUSA
; CURRENT FILING DATE: 2001-11-26
; PRIOR FILING DATE: US 09/177,039
; PRIOR FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-994-192-4

Query Match 100.0%; Score 797; DB 2; Length 797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLQKIASALMVLGSLPFAFDFTQDIRVEGLQRTPESTVFNLPVKVGDTYNDTHGSA 60
Db 1 MKLQKIASALMVLGSLPFAFDFTQDIRVEGLQRTPESTVFNLPVKVGDTYNDTHGSA 60

Qy 61 IIKSLIYATGFFDDYRVETADGQLLTWERTIGSLNITGAKMLQNDIAIKNLESFGLAQ 120
Db 61 IIKSLIYATGFFDDYRVETADGQLLTWERTIGSLNITGAKMLQNDIAIKNLESFGLAQ 120

Qy 121 SOYFNQATLNQAVAGLKEEYLGRGLNIQITPKVTKLARNRVDIITIDEGSKAKITDIE 180
Db 121 SOYFNQATLNQAVAGLKEEYLGRGLNIQITPKVTKLARNRVDIITIDEGSKAKITDIE 180

Qy 181 PEGNQVTSDRKLMQMSLTGEGGIWTLTRSNQFNEQKFAQDMKVTDFYQNGYFDFRIL 240
Db 181 PEGNQVTSDRKLMQMSLTGEGGIWTLTRSNQFNEQKFAQDMKVTDFYQNGYFDFRIL 240

Qy 241 DTDIQTNEDEKTKOTIKITVHEGGRFWGKVSIEGDTNEVPKAELEKLLTWKPGKWERQ 300
Db 241 DTDIQTNEDEKTKOTIKITVHEGGRFWGKVSIEGDTNEVPKAELEKLLTWKPGKWERQ 300
```

```

241 DTDIQTNEDEKTKOTIKITVHEGGRFWGKVSIEGDTNEVPKAELEKLLTWKPGKWERQ 300
301 MTAVLGEIQNRMGSAAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHITGNKT 360
301 MTAVLGEIQNRMGSAAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHITGNKT 360
361 RDEVVRELRQMESAPYDTSKLORSKERVLLCYFDNVQFDVPLAGTDPKVDLNNSLTE 420
361 RDEVVRELRQMESAPYDTSKLORSKERVLLCYFDNVQFDVPLAGTDPKVDLNNSLTE 420
421 RSTGSLDLGAGWQDVTGLVMSAGVSQDNLFCTGKSAALRASRSKTTLNGSLSFDPYFTA 480
421 RSTGSLDLGAGWQDVTGLVMSAGVSQDNLFCTGKSAALRASRSKTTLNGSLSFDPYFTA 480
481 DGVSGLDYVYGKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
481 DGVSGLDYVYGKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
541 YNKAPKHYADFTKKYCKTGTGSGFKGWLKGTGVGGRNKTDSALMPTRGYLTGVNAEIA 600
541 YNKAPKHYADFTKKYCKTGTGSGFKGWLKGTGVGGRNKTDSALMPTRGYLTGVNAEIA 600
601 LPSGKLQYYSATHNQTFWFFPLSKTFTMLGGEVGIAGGYGRTKEIPFFENFYGGGLGSVR 660
601 LPSGKLQYYSATHNQTFWFFPLSKTFTMLGGEVGIAGGYGRTKEIPFFENFYGGGLGSVR 660
661 GYESGTLGPRKYDVEYGEKISYGGNKANVSALLFPMGAKDARTVRLSLFADAGSVWDG 720
661 GYESGTLGPRKYDVEYGEKISYGGNKANVSALLFPMGAKDARTVRLSLFADAGSVWDG 720
721 KTYDDNSSSATGGRVONIYAGNTHKSTFTNELRYSAGGAVTWLSPLGPMKFRYAYPLKK 780
721 KTYDDNSSSATGGRVONIYAGNTHKSTFTNELRYSAGGAVTWLSPLGPMKFRYAYPLKK 780
781 KPEDEIQRFQFQLGTTTF 797
781 KPEDEIQRFQFQLGTTTF 797

RESULT 2
US-09-994-192-2
; Sequence 2, Application US/09994192
; Patent No. 6610306
; GENERAL INFORMATION:
; APPLICANT: Judd, Ralph C.
; APPLICANT: Manning, Scott D.
; TITLE OF INVENTION: Omp85 Proteins of Neisseria gonorrhoeae and Neisseria meningitidis
; FILE REFERENCE: USBC147AUSA
; CURRENT APPLICATION NUMBER: US/09/994,192
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US 09/177,039
; PRIOR FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 792
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-09-994-192-2

Query Match 19.7%; Score 157; DB 2; Length 792;
Best Local Similarity 100.0%; Pred. No. 3.5e-152;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 332 TKTVDFVHLIEPGRKIYVNEIHITGNKTRDEVVRRELQMESAPYDTSKLQSKERVEL 391
Db 332 TKTVDFVHLIEPGRKIYVNEIHITGNKTRDEVVRRELQMESAPYDTSKLQSKERVEL 391

Qy 392 LGYFDNVQFADVPLAGTTPKVDLNNSLTERSTGSLDSAGVQDPTGLVMSAGVSQDNLF 451
Db 392 LGYFDNVQFADVPLAGTTPKVDLNNSLTERSTGSLDSAGVQDPTGLVMSAGVSQDNLF 451
```



QY 452 TGKSAALRASRKTTLNGSLSTFTDYPFTADGVSLGYD 488  
|||||  
Db 452 TGKSAALRASRKTTLNGSLSTFTDYPFTADGVSLGYD 488

## RESULT 3

US-09-489-039A-8163  
; Sequence 8163, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 8163  
; LENGTH: 94  
; TYPE: PRT  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-8163

Query Match 1.0%; Score 8; DB 2; Length 94;  
Best Local Similarity 100.0%; Pred. No. 6.8;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 727 SSSATGGR 734

Db 76 SSSATGGR 83

## RESULT 4

US-09-205-258-1092  
; Sequence 1092, Application US/09205258  
; Patent No. 6525174  
; GENERAL INFORMATION:  
; APPLICANT: Young et al.  
; TITLE OF INVENTION: 207 Human Secreted Proteins  
; FILE REFERENCE: P2007P1  
; CURRENT APPLICATION NUMBER: US/09/205,258  
; CURRENT FILING DATE: 1998-12-04  
; EARLIER APPLICATION NUMBER: PCT/US98/11422  
; EARLIER FILING DATE: 1998-06-04  
; EARLIER APPLICATION NUMBER: 60/048,885  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/049,375  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,881  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,880  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,896  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/049,020  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,876  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,895  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,884  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,894  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,971  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,964  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,882  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,899

; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,893  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,900  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,901  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,892  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,915  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/049,019  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,970  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,972  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,916  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/049,373  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,875  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/049,374  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,917  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,949  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,974  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,883  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,897  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,898  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,962  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,963  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,877  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,878  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/070,923  
; EARLIER FILING DATE: 1997-12-18  
; EARLIER APPLICATION NUMBER: 60/092,921  
; EARLIER FILING DATE: 1998-07-15  
; EARLIER APPLICATION NUMBER: 60/094,657  
; EARLIER FILING DATE: 1998-07-30  
; NUMBER OF SEQ ID NOS: 1227  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 1092  
; LENGTH: 97  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (73)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-205-258-1092

Query Match 1.0%; Score 8; DB 2; Length 97;  
Best Local Similarity 100.0%; Pred. No. 7;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 756 SAGGAVTW 763

Db 14 SAGGAVTW 21

RESULT 5

```
US-10-004-860-1092
; Sequence 1092, Application US/10004860
; Patent No. 6914047
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/10/004,860
; CURRENT FILING DATE: 2001-12-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1092
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (73)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-004-860-1092

Query Match          1.0%; Score 8; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 756 SAGGAVTW 763
Db 14 SAGGAVTW 21
|||||

RESULT 6
US-09-270-767-45805
; Sequence 45805, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45805
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-45805

Query Match          1.0%; Score 8; DB 2; Length 230;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 589 RGYLTGVN 596
Db 188 RGYLTGVN 195
|||||

RESULT 7
US-09-902-540-15552
; Sequence 15552, Application US/09902540
; Patent No. 683447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR FILING DATE: 2000-07-10
; PRIOR FILING DATE: 2000-07-10

US-10-004-860-1092
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 15552
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-15552

Query Match          1.0%; Score 8; DB 2; Length 274;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 281 KAELEKLL 288
Db 177 KAELEKLL 184
|||||

RESULT 8
US-09-252-991A-24628
; Sequence 24628, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24628
; LENGTH: 848
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24628

Query Match          1.0%; Score 8; DB 2; Length 648;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 74 VRVETADG 81
Db 94 VRVETADG 101
|||||

RESULT 9
US-09-543-681A-4998
; Sequence 4998, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 4998
; LENGTH: 1589
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-4998

Query Match          1.0%; Score 8; DB 2; Length 1589;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 78 TADGQLLL 85
|||||
```

Db 563 TADQQLLL 570

RESULT 10

US-09-674-973A-147  
; Sequence 147, Application US/09674973A  
; Patent No. 6759046  
; GENERAL INFORMATION:  
; APPLICANT: No. 6759046sk Hydro ASA  
; TITLE OF INVENTION: Peptides  
; FILE REFERENCE: 26625-296  
; CURRENT APPLICATION NUMBER: US/09/674,973A  
; CURRENT FILING DATE: 2001-06-04  
; NUMBER OF SEQ ID NOS: 459  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 147  
; LENGTH: 23  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-674-973A-147

Query Match 0.9%; Score 7; DB 2; Length 23;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 283 ELEKLLT 289

Db 5 ELEKLLT 11

RESULT 11

US-08-971-089-10  
; Sequence 10, Application US/08971089  
; Patent No. 6376174  
; GENERAL INFORMATION:  
; APPLICANT: Pulst, Stefan M.  
; APPLICANT: Soles, Daniel R.  
; TITLE OF INVENTION: NUCLEIC ACID ENCODING  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CAMPBELL & FLORES, LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/971,089  
; FILING DATE:  
; CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/030,987  
; FILING DATE: 15-NOV-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ramos, Robert T.  
; REGISTRATION NUMBER: 37,915  
; REFERENCE/DOCKET NUMBER: P-CE 2862  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619)535-9001  
; TELEFAX: (619)535-8949  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 58 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-08-971-089-10

Query Match 0.9%; Score 7; DB 2; Length 58;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 458 LRASRSK 464

Db 4 LRASRSK 10

RESULT 12

US-10-117-604A-10  
; Sequence 10, Application US/10117604A  
; Patent No. 6960650  
; GENERAL INFORMATION:  
; APPLICANT: Pulst, Stefan M.  
; APPLICANT: Soles, Daniel R.  
; TITLE OF INVENTION: Nucleic Acid Encoding  
; TITLE OF INVENTION: Schwannomin-Binding-Proteins and Products Related Thereto  
; FILE REFERENCE: 66783-101  
; CURRENT APPLICATION NUMBER: US/10/117,604A  
; CURRENT FILING DATE: 2002-04-04  
; PRIOR APPLICATION NUMBER: US 60/030,987  
; PRIOR FILING DATE: 1996-11-15  
; PRIOR APPLICATION NUMBER: US 08/971,089  
; PRIOR FILING DATE: 1997-11-14  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 58  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-117-604A-10

Query Match 0.9%; Score 7; DB 2; Length 58;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 458 LRASRSK 464

Db 4 LRASRSK 10

RESULT 13

US-09-513-999C-7231  
; Sequence 7231, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; Patent No. 6783961  
; FILE REFERENCE: 59.US2.REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 7231  
; LENGTH: 60  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: 51  
; OTHER INFORMATION: Xaa=Ile or Leu or Val

US-09-513-999C-7231

Query Match 0.9%; Score 7; DB 2; Length 60;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 458 LRASRSK 464
    |||||
Db 38 LRASRSK 44

RESULT 14
US-09-328-352-6252
; Sequence 6252, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6252
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6252

Query Match 0.9%; Score 7; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 654 GGLGSVR 660
    |||||
Db 18 GGLGSVR 24

RESULT 15
US-09-489-039A-10485
; Sequence 10485, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 10485
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10485

Query Match 0.9%; Score 7; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 483 VSLGYDV 489
    |||||
Db 71 VSLGYDV 77

Search completed: April 12, 2006, 16:24:37
Job time : 57 secs

```

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 12, 2006, 16:19:27 ; Search time 44 Seconds  
(without alignments)  
1742.835 Million cell updates/sec

Title: US-10-606-618-4  
Perfect score: 797  
Sequence: 1 MKLKQTASALMLGISPLAF.....LKKKPEIQRFQQLGTTT 797

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.70

Searched: 283416 seqs, 96216763 residues

Word size : 1

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : PIR 80.\*

- 1: PIR1.\*
- 2: PIR2.\*
- 3: PIR3.\*
- 4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	752	94.4	797	2 D82000	outer membrane pro
2	752	94.4	797	2 G81228	outer membrane pro
3	752	94.4	797	2 T46206	hypothetical prote
4	9	1.1	328	2 T49132	hypothetical prote
5	8	1.0	435	2 A96984	hypothetical prote
6	8	1.0	129	2 A96984	hypothetical prote
7	8	1.0	225	2 E84423	glycerate dehydrog
8	8	1.0	335	2 B75057	formate dehydrogen
9	8	1.0	337	2 C82190	probable transamin
10	8	1.0	376	2 A71175	probable transamin
11	8	1.0	426	2 T04985	flagellar hook-len
12	8	1.0	429	2 G42365	site-specific reco
13	8	1.0	474	1 IMBP4	probable glycosyl
14	8	1.0	583	2 G83375	dynam-in-related pr
15	8	1.0	903	2 JE0327	dynam-in-related pr
16	8	1.0	903	2 T50334	insulin-like growt
17	8	1.0	1363	2 T43220	hemolysin A precu
18	8	1.0	1577	2 A35140	hypothetical prote
19	8	1.0	4919	2 T31105	hypothetical prote
20	7	0.9	75	2 E85707	probable regulator
21	7	0.9	76	1 CEBCDC	cell division cont
22	7	0.9	95	2 T25611	hypothetical prote
23	7	0.9	101	2 T33316	hypothetical prote
24	7	0.9	101	2 T35232	hypothetical prote
25	7	0.9	109	2 E72527	pimi protein - mou
26	7	0.9	118	2 S14079	hypothetical prote
27	7	0.9	131	2 A87461	hypothetical prote
28	7	0.9	148	2 T52550	probable transcrip
29	7	0.9	150	2 D81314	small protein B ho

hypothetical prote  
hypothetical prote  
hypothetical prote  
f42h10.6 protein -  
T-cell receptor ga  
probable acetyltra  
probable acyltrans  
probable efflux tr  
membrane fusion pr  
probable ATP-bind  
hypothetical prote  
hypothetical prote  
conserved hypochet  
hypothetical prote  
probable lipoprote  
probable integral  
conserved hypochet  
proteasome endopep  
lacyl-carrier-prot  
hypothetical prote  
hypothetical prote  
transcription regu  
probable transcrip  
hypothetical prote  
hypothetical prote  
hypothetical prote  
capsid protein - b  
pariplasmic flagel  
delta-aminolevulin  
hypothetical prote  
hypothetical prote  
gcpE protein [impo  
conserved hypochet  
poly (3-hydroxybut  
cytochrome c oxida  
hypothetical prote  
3-isopropylmalate  
enolase (eno) homo  
PDS1 protein - Yea  
RING finger-contai  
oligopeptide trans  
cyclin A-type (clo  
recombination prot  
ribonucleoside-tri  
conserved hypochet  
hypothetical prote  
phosphoglycerate k  
cell division cont  
N-ethylammelne ch  
lactose-binding pr  
hypothetical prote  
multidrug resistan  
probable cell divi  
hypothetical prote  
hypothetical prote  
hypothetical prote  
RNA-polymerase sig  
hypothetical prote  
probable membrane  
probable membrane  
helicase homolog H  
site-specific reco  
probable membrane  
cytochrome P450 Rv  
hypothetical prote  
site-specific DNA-  
hypothetical prote  
hypothetical prote  
hypothetical prote  
ATP-dependent RNA  
poliovirus recepto  
orc / cell divisio

103	7	0.9	521	2	A86909	hypothetical prote	176	6	0.8	70	2	G91236	50S ribosomal subu
104	7	0.9	526	1	KRBOVI	keratin, 54K type	177	6	0.8	70	2	G86083	50S ribosomal subu
105	7	0.9	537	2	T38015	hypothetical prote	178	6	0.8	71	2	E69345	SSU ribosomal prot
106	7	0.9	545	2	A80290	probable membrane	179	6	0.8	72	1	B24033	small acid-soluble
107	7	0.9	562	2	S61295	heat shock protein	180	6	0.8	74	2	AI0349	conserved hypotet
108	7	0.9	564	2	H82319	conserved hypotet	181	6	0.8	74	2	AB2071	hypothetical prote
109	7	0.9	587	2	JC5300	Ran GTPase activat	182	6	0.8	76	2	A48784	Ig kappa V regions
110	7	0.9	589	2	T52070	RNAL protein homol	183	6	0.8	76	2	B88318	protein age-1 limp
111	7	0.9	589	2	A36983	RNAL homolog fugu	184	6	0.8	76	2	F70241	hypothetical prote
112	7	0.9	619	2	S40938	hypothetical prote	185	6	0.8	77	2	AC2101	lipoprotein [impor
113	7	0.9	620	2	S38994	origin recognition	186	6	0.8	78	2	A64450	ribosomal protein
114	7	0.9	623	2	AD2295	hypothetical prote	187	6	0.8	78	2	AF2345	hypothetical prote
115	7	0.9	625	2	A72592	glutamine-fructose	188	6	0.8	79	2	S68245	phosphatidylcholin
116	7	0.9	649	1	H64476	lipoteate protein li	189	6	0.8	79	2	F70013	hypothetical prote
117	7	0.9	656	2	H84649	probable DnaJ prot	190	6	0.8	80	2	G81108	hypothetical prote
118	7	0.9	666	2	D82386	methyl-accepting c	191	6	0.8	80	2	A32364	photosystem I iron
119	7	0.9	728	2	S71467	diacylglycerol kin	192	6	0.8	80	2	G97805	hypothetical prote
120	7	0.9	745	2	D96829	homeobox protein (	193	6	0.8	81	1	FEPM15	photosystem I iron
121	7	0.9	747	2	S71478	homeotic protein A	194	6	0.8	81	1	FERZA	photosystem I iron
122	7	0.9	771	2	T01315	hypothetical prote	195	6	0.8	81	1	FEWT1	photosystem I iron
123	7	0.9	784	2	E82731	outer membrane ant	196	6	0.8	81	1	FEZW1C	photosystem I iron
124	7	0.9	797	2	H83190	probable outer mem	197	6	0.8	81	2	S07170	photosystem I iron
125	7	0.9	812	2	AH1049	ribonuclease R (RN	198	6	0.8	81	2	S73295	photosystem I iron
126	7	0.9	823	2	T52425	kinesin-like prote	199	6	0.8	81	2	T07571	photosystem I iron
127	7	0.9	827	1	S56404	virulence-associat	200	6	0.8	81	2	S12198	photosystem I iron
128	7	0.9	827	2	C86114	probable enzyme va	201	6	0.8	81	2	AI3461	hypothetical prote
129	7	0.9	827	2	C91273	probable enzyme [i	202	6	0.8	81	2	A98247	hypothetical prote
130	7	0.9	856	2	F96998	phosphoenolpyruvat	203	6	0.8	81	2	H97567	hypothetical prote
131	7	0.9	881	2	I84737	kinesin heavy chai	204	6	0.8	83	2	F81267	30S ribosomal prot
132	7	0.9	888	2	D96619	protein T30E16.9 [	205	6	0.8	83	2	S77417	protochlorophyllid
133	7	0.9	942	2	T19553	hypothetical prote	206	6	0.8	83	2	AI0032	probable type III
134	7	0.9	953	1	B30169	leukotoxin A - Pas	207	6	0.8	84	2	E97807	hypothetical prote
135	7	0.9	963	1	A41919	kinesin heavy chai	208	6	0.8	85	2	T08595	cysteine proteinas
136	7	0.9	983	2	AG2381	glycine cleavage s	209	6	0.8	85	2	AI0316	sec-independent pr
137	7	0.9	1054	2	D70425	conserved hypotet	210	6	0.8	86	2	H85939	type III secretion
138	7	0.9	1088	2	A69493	cysteine proteinas	211	6	0.8	86	2	D91094	type III secretion
139	7	0.9	1121	2	JC7329	WD-repeat protein	212	6	0.8	86	2	QJ0730	9K protein - prote
140	7	0.9	1221	2	T25005	hypothetical prote	213	6	0.8	86	2	E82985	hypothetical prote
141	7	0.9	1222	2	B90593	hypothetical prote	214	6	0.8	86	2	AG3442	helix-turn-helix p
142	7	0.9	1234	2	T31623	hypothetical prote	215	6	0.8	87	2	T05709	auxin-induced prot
143	7	0.9	1259	2	T32901	hypothetical prote	216	6	0.8	88	2	C82468	hypothetical prote
144	7	0.9	1366	2	C85077	probable polyprote	217	6	0.8	88	2	E70880	hypothetical prote
145	7	0.9	1434	2	T30172	transmembrane prot	218	6	0.8	90	2	S15149	hypothetical prote
146	7	0.9	1442	2	T18538	patched protein -	219	6	0.8	90	2	B82799	hypothetical prote
147	7	0.9	1449	2	B81963	IgA-specific serin	220	6	0.8	91	2	S17627	Ig kappa chain v r
148	7	0.9	1457	2	D81019	adhesion and penet	221	6	0.8	91	2	S17629	Ig kappa chain v r
149	7	0.9	1513	2	T44045	hypothetical prote	222	6	0.8	91	2	S17638	Ig kappa chain v r
150	7	0.9	1520	2	T44231	hypothetical prote	223	6	0.8	91	2	S17639	Ig kappa chain v r
151	7	0.9	1658	2	D75489	hypothetical prote	224	6	0.8	91	2	S17628	Ig kappa chain v r
152	7	0.9	1943	2	B64596	toxin-like outer m	225	6	0.8	91	2	S17637	Ig kappa chain v r
153	7	0.9	2174	2	E95965	hypothetical glyci	226	6	0.8	93	2	B69190	hypothetical prote
154	7	0.9	2274	2	T30258	adenomatous polypo	227	6	0.8	93	2	G71370	probable ribosomal
155	7	0.9	2431	1	MNVVSF	nonstructural poly	228	6	0.8	93	2	D70192	chaperonin (groES)
156	7	0.9	2478	2	AH2140	polyketide synthas	229	6	0.8	94	2	A60097	cortical cytoskele
157	7	0.9	3194	2	D71917	toxin-like outer m	230	6	0.8	94	2	S32105	chaperonin groES -
158	7	0.9	4385	2	T29042	hypothetical prote	231	6	0.8	94	2	JN0660	heat shock protein
159	7	0.9	4485	2	T08044	dynein gamma heavy	232	6	0.8	94	2	B40506	PRF2 protein - hum
160	7	0.9	5369	2	T44807	mycosubtilin synth	233	6	0.8	94	2	S75365	hypothetical prote
161	6	0.8	17	2	I55612	thyroid hormone re	234	6	0.8	95	2	D33730	Ig kappa chain v r
162	6	0.8	23	2	S45030	homeotic protein S	235	6	0.8	95	2	T03068	hypothetical prote
163	6	0.8	23	2	S60569	homeodomain protei	236	6	0.8	96	2	B26074	cysteine proteinas
164	6	0.8	25	2	D41606	homeotic protein M	237	6	0.8	96	2	S34937	heat shock protein
165	6	0.8	52	2	A12399	hypothetical prote	238	6	0.8	96	2	C82048	chaperonin, 10 kD
166	6	0.8	57	2	AB0373	hypothetical prote	239	6	0.8	96	2	JC4518	heat-shock protein
167	6	0.8	60	2	F75338	hypothetical prote	240	6	0.8	96	2	H97048	hypothetical prote
168	6	0.8	62	2	G70988	hypothetical prote	241	6	0.8	97	2	S26341	Ig light chain v r
169	6	0.8	65	2	H82773	hypothetical prote	242	6	0.8	97	2	PH1084	Ig light chain v r
170	6	0.8	66	2	AF3083	hypothetical prote	243	6	0.8	97	2	C64029	hypothetical prote
171	6	0.8	67	2	F85904	hypothetical prote	244	6	0.8	97	2	F82416	hypothetical prote
172	6	0.8	68	2	H90086	hypothetical prote	245	6	0.8	98	2	H82577	hypothetical prote
173	6	0.8	68	2	F84002	hypothetical prote	246	6	0.8	99	2	S51210	Ig kappa chain v r
174	6	0.8	69	2	S33899	ribosomal protein	247	6	0.8	99	2	S53124	probable ribosomal
175	6	0.8	70	1	R5EC31	ribosomal protein	248	6	0.8	100	2	S29590	Ig kappa chain v r

249	6	0.8	100	2	S03636	homeotic protein H	322	6	0.8	126	2	D95410	hypothetical prote
250	6	0.8	101	2	F92421	conserved hypotet	323	6	0.8	127	2	F75092	ssu ribosomal prot
251	6	0.8	101	2	C69076	hypothetical prote	324	6	0.8	127	2	D97381	methylglyoxal synt
252	6	0.8	102	2	S11115	ig kappa chain v r	325	6	0.8	127	2	AC2599	methylglyoxal synt
253	6	0.8	102	2	AF3346	SSU ribosomal prot	326	6	0.8	127	2	A75086	translation initia
254	6	0.8	102	2	H87403	ribosomal protein	327	6	0.8	128	2	S39678	ywbH protein - Bac
255	6	0.8	102	2	A23931	anti-lipoplysacch	328	6	0.8	128	2	F84216	hypothetical prote
256	6	0.8	103	2	S29591	ig kappa chain v r	329	6	0.8	128	2	S53584	probable membrane
257	6	0.8	103	2	G75257	hypothetical prote	330	6	0.8	129	2	B72853	AcOrf-26 protein - Bom
258	6	0.8	104	2	B49049	ig kappa chain v r	331	6	0.8	129	2	T41771	AcMNPV orf26 - Bom
259	6	0.8	105	2	D95108	conserved hypotet	332	6	0.8	129	2	T46300	hypothetical prote
260	6	0.8	106	2	P50071	ig kappa chain v r	333	6	0.8	129	2	S45868	probable membrane
261	6	0.8	106	2	S11114	ig kappa chain v r	334	6	0.8	129	2	T36916	hypothetical prote
262	6	0.8	106	2	S11120	ig kappa chain v r	335	6	0.8	130	1	JL0079	ig kappa chain pre
263	6	0.8	106	2	G72059	conserved hypotet	336	6	0.8	130	1	JL0079	chorion class B pr
264	6	0.8	106	2	D86563	hypothetical prote	337	6	0.8	130	2	S01439	lens fiber membran
265	6	0.8	106	2	T24774	hypothetical prote	338	6	0.8	130	2	S01439	hypothetical prote
266	6	0.8	106	2	G27887	ig kappa chain v r	339	6	0.8	130	2	H83150	hypothetical prote
267	6	0.8	107	1	PXPSEP	putidaredoxin [val	340	6	0.8	131	1	S12972	amicyanin - Paraco
268	6	0.8	107	1	B36950	urease (EC 3.5.1.5	341	6	0.8	131	1	S12972	Mut7/nudix family
269	6	0.8	107	2	S11112	ig kappa chain v r	342	6	0.8	131	2	C87416	hypothetical prote
270	6	0.8	107	2	S11118	ig kappa chain v r	343	6	0.8	131	2	B71055	ribosomal protein
271	6	0.8	107	2	S11116	ig kappa chain v r	344	6	0.8	132	2	C70161	hypothetical prote
272	6	0.8	107	2	P00111	ig kappa chain v r	345	6	0.8	132	2	D72583	homeotic protein G
273	6	0.8	107	2	S11113	ig kappa chain v r	346	6	0.8	132	2	S39540	hypothetical prote
274	6	0.8	107	2	P70395	ig kappa chain v r	347	6	0.8	133	2	T01042	hypothetical prote
275	6	0.8	107	2	P70402	ig kappa chain v r	348	6	0.8	134	2	C69849	hypothetical prote
276	6	0.8	107	2	S11119	ig kappa chain v r	349	6	0.8	135	2	AF2055	hypothetical prote
277	6	0.8	107	2	P70397	ig kappa chain v r	350	6	0.8	135	2	B72768	hypothetical prote
278	6	0.8	107	2	S11123	ig kappa chain v r	351	6	0.8	136	2	T49582	positive regulatio
279	6	0.8	107	2	P70398	ig kappa chain v r	352	6	0.8	136	2	T49582	hypothetical prote
280	6	0.8	107	2	S11121	ig kappa chain v r	353	6	0.8	137	2	T45079	hypothetical prote
281	6	0.8	107	2	S11117	ig kappa chain v r	354	6	0.8	137	2	A69219	hypothetical prote
282	6	0.8	107	2	A30562	ig kappa chain v r	355	6	0.8	138	2	B83135	hypothetical prote
283	6	0.8	107	2	P70406	ig kappa chain v r	356	6	0.8	138	2	G85806	hypothetical prote
284	6	0.8	107	2	B30562	ig kappa chain v r	357	6	0.8	139	2	A82140	probable isomerase
285	6	0.8	107	2	P70405	ig kappa chain v r	358	6	0.8	139	2	H97449	homeobox-contains
286	6	0.8	107	2	T17701	hypothetical prote	359	6	0.8	140	2	E97462	organic hydroperox
287	6	0.8	108	2	C48078	biliary glycoprote	360	6	0.8	140	2	AG2680	hemoglobin alpha-I
288	6	0.8	108	2	G30560	ig kappa chain v r	361	6	0.8	141	1	HALZC	kinesin heavy chai
289	6	0.8	109	2	C30515	ig heavy chain v r	362	6	0.8	143	2	A69115	DNA transport mach
290	6	0.8	109	2	D91085	hypothetical prote	363	6	0.8	143	2	E30338	transposase IS240-
291	6	0.8	109	2	F85930	hypothetical prote	364	6	0.8	143	2	B69267	trypanothione-glut
292	6	0.8	109	2	D65061	hypothetical prote	365	6	0.8	143	2	S58429	conserved hypotet
293	6	0.8	109	2	AH3240	conserved hypotet	366	6	0.8	143	2	AG2682	hypothetical prote
294	6	0.8	110	2	S51383	probable membrane	367	6	0.8	143	2	E97464	probable Sdhb subu
295	6	0.8	111	2	G85974	suppressor protein	368	6	0.8	144	2	D70843	hypothetical prote
296	6	0.8	111	2	G91129	genome polyprotein	369	6	0.8	144	2	C72668	hypothetical prote
297	6	0.8	112	2	S51121	polyprotein - hepa	370	6	0.8	145	2	T36527	major tail shaft p
298	6	0.8	113	2	PQ0274	polyprotein - hepa	371	6	0.8	145	2	AD1447	heat shock protein
299	6	0.8	113	2	PQ0273	xis 5'-region hypo	372	6	0.8	145	2	F69214	conserved hypotet
300	6	0.8	113	2	A55205	transcription fact	373	6	0.8	145	2	F90185	hypothetical prote
301	6	0.8	114	2	I51025	conserved hypotet	374	6	0.8	145	2	S26443	calmodulin-like pr
302	6	0.8	114	2	E97976	hypothetical prote	375	6	0.8	146	2	T51473	hypothetical prote
303	6	0.8	115	2	T29883	hypothetical prote	376	6	0.8	146	2	T22474	hypothetical prote
304	6	0.8	117	2	H71431	probable minor cap	377	6	0.8	146	2	H64126	conserved hypotet
305	6	0.8	117	2	T13096	hypothetical prote	378	6	0.8	146	2	B82167	conserved hypotet
306	6	0.8	117	2	S75884	hypothetical prote	379	6	0.8	146	2	AE2935	hypothetical prote
307	6	0.8	119	2	A64249	ribosomal protein	380	6	0.8	146	2	B98347	hypothetical prote
308	6	0.8	119	2	B84407	hypothetical prote	381	6	0.8	146	2	PH0127	ig heavy chain pre
309	6	0.8	120	2	S22049	reverse transcript	382	6	0.8	147	2	PH0127	ig heavy chain pre
310	6	0.8	120	2	AB2668	conserved hypotet	383	6	0.8	147	2	PH0131	ig heavy chain pre
311	6	0.8	120	2	AH1813	hypothetical prote	384	6	0.8	147	2	PH0131	ig heavy chain pre
312	6	0.8	121	2	H70471	conserved hypotet	385	6	0.8	147	2	PH0125	ig heavy chain pre
313	6	0.8	122	2	F97779	hypothetical prote	386	6	0.8	147	2	PH0125	ig heavy chain pre
314	6	0.8	123	2	G71189	hypothetical prote	387	6	0.8	147	2	PH0130	ig heavy chain pre
315	6	0.8	124	2	F82205	chemotaxis protein	388	6	0.8	147	2	A29910	myosin calcium-bin
316	6	0.8	124	2	G75172	hypothetical prote	389	6	0.8	147	2	T28131	hypothetical prote
317	6	0.8	124	2	AD3428	transposase BME114	390	6	0.8	150	2	A97536	hypothetical prote
318	6	0.8	124	2	S05005	homeotic protein H	391	6	0.8	151	2	T15428	hypothetical prote
319	6	0.8	125	2	C82831	ribosomal-binding	392	6	0.8	151	2	A75297	hypothetical prote
320	6	0.8	125	2	AC3195	hypothetical prote	393	6	0.8	152	2	S29752	ubiquitin-activati
321	6	0.8	125	2	T16848	hypothetical prote	394	6	0.8	153	1	JT0572	profilin - Tetrah

395	6	0.8	153	1	WRBP15	early protein gp17	468	6	0.8	178	2	A47071	hypothetical prote
396	6	0.8	153	1	C69847	conserved hypotet	469	6	0.8	179	2	A53522	pepidylprolyl iso
397	6	0.8	153	2	S63367	ribosomal protein	470	6	0.8	179	2	B65695	ribosomal protein
398	6	0.8	153	2	AH2203	bacterioferritin c	471	6	0.8	179	2	T48416	hypothetical prote
399	6	0.8	153	2	G70077	hypothetical prote	472	6	0.8	181	2	AD2427	hypothetical prote
400	6	0.8	153	2	S34255	hypothetical prote	473	6	0.8	181	2	E83436	probable oxidase P
401	6	0.8	153	2	C86324	protein F14D16.23	474	6	0.8	182	2	A02947	keratin, 60K type
402	6	0.8	154	2	T70881	hypothetical prote	475	6	0.8	182	2	A91031	probable fimbrial-
403	6	0.8	154	2	T34825	hypothetical prote	476	6	0.8	182	2	AH1579	hypothetical prote
404	6	0.8	155	2	T15379	hypothetical prote	477	6	0.8	182	2	G90235	hypothetical prote
405	6	0.8	156	2	F84356	hypothetical prote	478	6	0.8	183	2	A40360	hypothetical prote
406	6	0.8	156	2	AG0243	probable exported	479	6	0.8	183	2	C85786	hypothetical prote
407	6	0.8	157	2	F82390	methylated-DNA-[pr	480	6	0.8	183	2	G90937	hypothetical prote
408	6	0.8	159	2	D72886	hypothetical prote	481	6	0.8	183	2	S26961	H+-transporting tw
409	6	0.8	160	2	T11949	hypothetical prote	482	6	0.8	183	2	T37965	probable 40s ribos
410	6	0.8	161	2	JC7151	vacuolar H+-ATPase	483	6	0.8	183	2	B90092	hypothetical prote
411	6	0.8	161	2	F71860	biotin carboxyl ca	484	6	0.8	184	2	A05045	hypothetical prote
412	6	0.8	161	2	G71407	transcription fact	485	6	0.8	184	2	T33006	hypothetical prote
413	6	0.8	161	2	S50931	hypothetical prote	486	6	0.8	184	2	B71897	hypothetical prote
414	6	0.8	162	1	RPMNA	phycoerythrocyanin	487	6	0.8	185	2	G75379	conserved hypotet
415	6	0.8	162	2	T70314	hypothetical prote	488	6	0.8	185	2	A13454	hypothetical prote
416	6	0.8	164	1	D69783	transcription regu	489	6	0.8	185	2	T19073	probable pyruvate
417	6	0.8	164	2	AE1900	NADH dehydrogenase	490	6	0.8	186	2	T19073	hypothetical prote
418	6	0.8	165	2	D97283	ribosomal protein	491	6	0.8	186	2	AF3094	conserved hypotet
419	6	0.8	165	2	B72618	hypothetical prote	492	6	0.8	186	2	F90646	probable fimbrial
420	6	0.8	165	2	AG2428	hypothetical prote	493	6	0.8	186	2	F85497	probable fimbrial
421	6	0.8	166	2	S78003	cuticle structural	494	6	0.8	187	2	H95998	probable drpp-4-de
422	6	0.8	166	2	G90661	probable peptide c	495	6	0.8	187	2	D99192	hypothetical prote
423	6	0.8	166	2	E85512	probable peptide c	496	6	0.8	188	2	JU0451	hypothetical 21K p
424	6	0.8	166	2	E64748	translation releas	497	6	0.8	188	2	I59116	myc protein - huma
425	6	0.8	167	2	C71803	ubiquinol-cytochro	498	6	0.8	188	2	I79500	myc protein - huma
426	6	0.8	167	2	JM0065	fast skeletal trop	499	6	0.8	188	2	C97438	hypothetical prote
427	6	0.8	167	2	S07473	early light-induce	500	6	0.8	188	2	AF2656	conserved hypotet
428	6	0.8	167	2	AC0481	probable gluconoki	501	6	0.8	189	2	E95569	probable IAA6 prot
429	6	0.8	167	2	D55224	hypothetical prote	502	6	0.8	189	2	S58493	auxin-induced prot
430	6	0.8	167	2	G90175	NADH dehydrogenase	503	6	0.8	189	2	S70104	hypothetical prote
431	6	0.8	168	2	S41973	serine proteinase	504	6	0.8	190	2	AD3329	acetylactate synth
432	6	0.8	169	1	WQECF3	phosphotransferase	505	6	0.8	191	1	JH0585	ribosomal protein
433	6	0.8	169	1	H69136	hypothetical prote	506	6	0.8	191	2	B64597	adenylate kinase -
434	6	0.8	169	2	D85884	PTS system, glucos	507	6	0.8	191	2	C90518	recombination prot
435	6	0.8	169	2	A98040	glucose-specific P	508	6	0.8	191	2	H64887	probable phage-rel
436	6	0.8	169	2	T44852	molybdopterin co-f	509	6	0.8	191	2	E64909	probable phage-rel
437	6	0.8	169	2	I51903	type I interleukin	510	6	0.8	191	2	E72455	hypothetical prote
438	6	0.8	169	2	C70207	outer membrane pro	511	6	0.8	191	2	S74679	hypothetical prote
439	6	0.8	170	2	C75184	VP29-like phospho	512	6	0.8	191	2	I40153	outer surface prot
440	6	0.8	170	2	S53648	ribosomal protein	513	6	0.8	191	2	E84375	hypothetical prote
441	6	0.8	170	2	F87482	hypothetical prote	514	6	0.8	191	2	A64704	hypothetical prote
442	6	0.8	171	1	JBA041	chorion claes B pr	515	6	0.8	191	2	A71814	hypothetical prote
443	6	0.8	171	2	G70893	probable lpuU prot	516	6	0.8	192	2	S70267	outer surface prot
444	6	0.8	171	2	E87459	cytochrome c famil	517	6	0.8	192	2	T05159	hypothetical prote
445	6	0.8	172	2	E81897	probable host-nucl	518	6	0.8	193	2	E85693	probable tail fibe
446	6	0.8	172	2	S07474	early light-induce	519	6	0.8	193	2	C90835	tail fiber assembl
447	6	0.8	172	2	B83696	hypothetical prote	520	6	0.8	193	2	D81009	conserved hypotet
448	6	0.8	173	2	D90177	15S ribosomal prot	521	6	0.8	193	2	E82031	probable integral
449	6	0.8	173	2	B85875	probable minor fim	522	6	0.8	193	2	S70276	outer surface prot
450	6	0.8	173	2	A70914	hypothetical prote	523	6	0.8	193	2	S70287	outer surface prot
451	6	0.8	174	2	B75176	hypothetical prote	524	6	0.8	194	1	R5PM24	ribosomal protein
452	6	0.8	174	2	T03056	hypothetical prote	525	6	0.8	194	2	T16556	hypothetical prote
453	6	0.8	174	2	T27552	hypothetical prote	526	6	0.8	194	2	T52044	dof zinc finger pr
454	6	0.8	174	2	D86239	protein T10024.23	527	6	0.8	194	2	T20277	outer surface prot
455	6	0.8	175	2	JC7274	DNA binding protei	528	6	0.8	194	2	T20322	hypothetical prote
456	6	0.8	175	2	C39141	transcription repr	529	6	0.8	195	2	AE1823	hypothetical prote
457	6	0.8	175	2	AB2297	conserved hypotet	530	6	0.8	195	2	G83170	hypothetical prote
458	6	0.8	176	2	AD1174	conserved hypotet	531	6	0.8	196	2	B86653	hypothetical prote
459	6	0.8	176	2	AE1531	conserved hypotet	532	6	0.8	196	2	C64891	ferriphyochelin-bin
460	6	0.8	177	2	F83114	50S ribosomal prot	533	6	0.8	196	2	AH2441	hypothetical prote
461	6	0.8	178	2	G91182	probable fimbrial	534	6	0.8	196	2	G97964	conserved hypotet
462	6	0.8	178	2	C86029	probable major fim	535	6	0.8	196	2	AB1601	ctd-p-glucose 4-6-d
463	6	0.8	178	2	B95183	non-heme iron-cont	536	6	0.8	197	2	JC3239	neutrophil gelatin
464	6	0.8	178	2	E98050	hypothetical prote	537	6	0.8	198	2	S72709	lepb170_C3_229 pr
465	6	0.8	178	2	T01890	hypothetical prote	538	6	0.8	198	2	A25706	sorcin - Chinese h
466	6	0.8	178	2	I40104	outer surface prot	539	6	0.8	198	2	S52094	sorcin - human
467	6	0.8	178	2	I40125	outer surface prot	540	6	0.8	199	2	C96570	hypothetical prote



541	adenylylsulfate ki	614	6	0.8	221	2	A72097
542	lipocalin - mouse	615	6	0.8	221	2	G86525
543	transcription init	616	6	0.8	221	2	T15999
544	transcription init	617	6	0.8	222	2	F72572
545	hypothetical prote	618	6	0.8	222	2	H82794
546	hypothetical prote	619	6	0.8	222	2	H87380
547	receptor like prot	620	6	0.8	222	2	S62001
548	probable two-compo	621	6	0.8	223	2	A84436
549	probable two-compo	622	6	0.8	223	2	T36952
550	hypothetical prote	623	6	0.8	223	2	S73367
551	hypothetical prote	624	6	0.8	223	2	E89567
552	acetyltransferase	625	6	0.8	224	2	AG1196
553	holliday junction	626	6	0.8	224	2	S31845
554	hypothetical prote	627	6	0.8	225	1	SYECDB
555	probable glycosida	628	6	0.8	225	2	A99206
556	sex-determining pr	629	6	0.8	226	2	H87518
557	5-bromo-4-chloroin	630	6	0.8	226	2	AH3080
558	probable peptide c	631	6	0.8	226	2	S23280
559	hypothetical prote	632	6	0.8	227	1	ADMSC
560	probable two-compo	633	6	0.8	227	2	A38452
561	croate phosphorib	634	6	0.8	227	2	T49711
562	conserved hypotet	635	6	0.8	228	2	E82408
563	hypothetical prote	636	6	0.8	228	2	T37026
564	glutathione transf	637	6	0.8	228	2	C90276
565	interleukin-6 - sh	638	6	0.8	230	2	T34822
566	2-dehydro-3-deoxy-	639	6	0.8	230	2	C64396
567	glutathione transf	640	6	0.8	230	2	E71224
568	outer surface prot	641	6	0.8	231	2	AG2277
569	hypothetical prote	642	6	0.8	231	2	AE2297
570	hypothetical prote	643	6	0.8	232	2	S75699
571	DNA-directed DNA p	644	6	0.8	232	2	H72807
572	probable 2-dehydro	645	6	0.8	233	2	S15960
573	imidazoleglycerol-	646	6	0.8	233	2	T28914
574	transcription regu	647	6	0.8	234	2	T06995
575	probable acetyltra	648	6	0.8	234	2	H81669
576	hypothetical prote	649	6	0.8	234	2	T20933
577	sarcoma amplified	650	6	0.8	235	2	E69814
578	VPS29-like phospho	651	6	0.8	235	2	S25058
579	ribosomal protein	652	6	0.8	235	2	T36923
580	hypothetical prote	653	6	0.8	236	2	S16164
581	hypothetical prote	654	6	0.8	236	2	S35766
582	hypothetical prote	655	6	0.8	236	2	S41326
583	hypothetical prote	656	6	0.8	236	2	QJ2298
584	hypothetical prote	657	6	0.8	237	2	C84065
585	hypothetical prote	658	6	0.8	237	2	S47351
586	hypothetical prote	659	6	0.8	238	2	A97336
587	serine esterase [i	660	6	0.8	238	2	A10077
588	myb-related transc	661	6	0.8	239	2	A75293
589	hypothetical prote	662	6	0.8	239	2	T51534
590	cytochrome b561 At	663	6	0.8	240	2	S75021
591	hypothetical prote	664	6	0.8	240	2	H90778
592	two component resp	665	6	0.8	241	2	T00751
593	YagE family [impor	666	6	0.8	242	2	H69885
594	yage family - Chla	667	6	0.8	242	2	C85840
595	ribosomal protein	668	6	0.8	242	2	G87696
596	hypothetical prote	669	6	0.8	242	2	A43904
597	hypothetical prote	670	6	0.8	243	1	B86746
598	adenylate kinase (	671	6	0.8	243	2	B71512
599	hypothetical prote	672	6	0.8	243	2	A43596
600	hypothetical prote	673	6	0.8	243	2	A69225
601	hypothetical prote	674	6	0.8	243	2	JC7596
602	transcription fact	675	6	0.8	244	1	RDECPA
603	2-keto-3-deoxy-6-p	676	6	0.8	244	2	B64003
604	GRP-binding protei	677	6	0.8	244	2	B69381
605	conserved hypotet	678	6	0.8	245	2	B82286
606	hypothetical prote	679	6	0.8	245	2	AB8738
607	MADS-box protein I	680	6	0.8	246	2	AC3024
608	probable transcrip	681	6	0.8	246	2	T00704
609	potential acrer/en	682	6	0.8	246	2	S74961
610	probable transcrip	683	6	0.8	247	2	G83382
611	hypothetical prote	684	6	0.8	247	2	D69453
612	hypothetical prote	685	6	0.8	247	2	G64788
613	hypothetical prote	686	6	0.8	248	2	F69449

687	6	0.8	248	2	I64230	sensory rhodopsin	760	6	0.8	266	2	T25230	hypothetical prote
688	6	0.8	249	1	A30113	NADH2 dehydrogenas	761	6	0.8	266	2	T22185	hypothetical prote
689	6	0.8	249	1	B30113	NADH2 dehydrogenas	762	6	0.8	267	2	H86320	probable MYB47 tra
690	6	0.8	249	2	AF1405	creatine amidoxy	763	6	0.8	267	2	E64175	hypothetical prote
691	6	0.8	249	2	AF1781	creatine amidoxy	764	6	0.8	267	2	H83232	probable ATP-bindi
692	6	0.8	250	2	H95161	conserved hypochet	765	6	0.8	267	2	S74998	hypothetical prote
693	6	0.8	250	2	G98027	conserved hypochet	766	6	0.8	267	2	E75471	transcription regu
694	6	0.8	250	2	G72650	hypothetical prote	767	6	0.8	267	2	A46122	homeotic protein H
695	6	0.8	250	2	D75119	hypothetical prote	768	6	0.8	267	2	A49068	cranosynotosis-as
696	6	0.8	251	2	H76668	luteinizing hormon	769	6	0.8	268	1	A49473	glutamate racemase
697	6	0.8	251	2	H65007	VacJ lipoprotein p	770	6	0.8	268	2	S31010	gene 65 protein -
698	6	0.8	251	2	E91032	lipoprotein precur	771	6	0.8	268	2	T46980	hypothetical prote
699	6	0.8	251	2	F85876	lipoprotein precur	772	6	0.8	268	2	AE0241	conserved hypochet
700	6	0.8	251	2	F70412	dihydroorotate deh	773	6	0.8	268	2	S18814	homeotic protein H
701	6	0.8	252	2	C95183	triosephosphate is	774	6	0.8	269	2	T16115	hypothetical prote
702	6	0.8	252	2	A28449	tropomyosin, cytos	775	6	0.8	269	2	B84013	hypothetical prote
703	6	0.8	252	2	T10697	immature seed prot	776	6	0.8	269	2	T26504	hypothetical prote
704	6	0.8	253	2	H69219	pyroline-5-carbox	777	6	0.8	270	1	CC8C1D	cell division inhi
705	6	0.8	253	2	QJ2255	triose-phosphate i	778	6	0.8	270	2	B84968	septum site-determ
706	6	0.8	253	2	S44053	structural protein	779	6	0.8	270	2	AH0724	septum site-determ
707	6	0.8	253	2	F69134	hypothetical prote	780	6	0.8	270	2	F85695	cell division inhi
708	6	0.8	253	2	G81311	probable ATP/GTP-b	781	6	0.8	270	2	E90837	cell division inhi
709	6	0.8	253	2	AI3598	transposase BMS10	782	6	0.8	270	2	AE0253	septum site-determ
710	6	0.8	254	2	B87336	DNA-binding respon	783	6	0.8	270	2	S71793	head-inducing fact
711	6	0.8	254	2	T08476	inclusion membrane	784	6	0.8	271	2	C81230	septum site-determ
712	6	0.8	254	2	E84382	hypothetical prote	785	6	0.8	271	2	QJ0950	ICP 18.5 protein -
713	6	0.8	254	2	C81208	ABC transporter, A	786	6	0.8	271	2	B60176	hypothetical prote
714	6	0.8	254	2	H81784	probable ABC trans	787	6	0.8	272	2	C75548	hypothetical prote
715	6	0.8	255	1	T5ECT	triose-phosphate 1	788	6	0.8	273	2	AH2709	transcription regu
716	6	0.8	255	2	A35255	chlorocatechol 1,2	789	6	0.8	273	2	S12637	transposase - Esch
717	6	0.8	255	2	AD0940	triosephosphate is	790	6	0.8	273	2	F69199	conserved hypochet
718	6	0.8	255	2	AE0011	triose-phosphate 1	791	6	0.8	273	2	S23281	homeotic protein m
719	6	0.8	255	2	D91234	triosephosphate is	792	6	0.8	274	2	A61030	nitrogenase (EC 1.
720	6	0.8	255	2	D86081	triosephosphate is	793	6	0.8	274	2	A43719	ured protein - Pro
721	6	0.8	255	2	AI1374	conserved hypochet	794	6	0.8	275	1	S78606	porin - slime mold
722	6	0.8	255	2	AG1744	conserved hypochet	795	6	0.8	275	2	S27805	signal peptidase I
723	6	0.8	255	2	C90431	conserved hypochet	796	6	0.8	275	2	S66062	signal peptidase-1
724	6	0.8	255	2	B87595	transcription regu	797	6	0.8	275	2	E83655	hypothetical prote
725	6	0.8	256	2	C98869	trans-2-enoyl-ACP	798	6	0.8	275	2	S05299	adenyl-ly-sulfate k
726	6	0.8	256	2	A54322	corticotropin / li	799	6	0.8	276	1	S47640	ketocacyl reductase
727	6	0.8	256	2	H69348	hypothetical prote	800	6	0.8	276	2	T29125	hypothetical prote
728	6	0.8	256	2	E95936	guflA protein homol	801	6	0.8	276	2	E83922	halorhodopsin [sai
729	6	0.8	257	1	S22363	guflA protein homol	802	6	0.8	276	2	T48842	septum site-determ
730	6	0.8	257	2	H91119	guflA protein homol	803	6	0.8	276	2	C82136	hypothetical prote
731	6	0.8	257	2	G85964	heat shock protein	804	6	0.8	276	2	T38825	hypothetical prote
732	6	0.8	258	1	C69175	hypothetical prote	805	6	0.8	277	1	H71220	malD protein - Str
733	6	0.8	258	2	C94758	hypothetical prote	806	6	0.8	277	2	S32571	conserved hypochet
734	6	0.8	258	2	T27333	hypothetical prote	807	6	0.8	277	2	H87213	hypothetical prote
735	6	0.8	259	2	H86809	oxidoreductase ypa	808	6	0.8	277	2	S03240	hypothetical prote
736	6	0.8	259	2	G98050	triose-phosphate 1	809	6	0.8	277	2	E72564	hypothetical prote
737	6	0.8	259	2	J50660	homeotic protein H	810	6	0.8	277	2	G97783	phytoene synthase
738	6	0.8	259	2	A38284	hypothetical prote	811	6	0.8	277	2	AD3386	plant-metabolite d
739	6	0.8	260	2	S70599	cytochrome-c oxida	812	6	0.8	278	2	A84131	hypothetical prote
740	6	0.8	260	2	AB2536	hypothetical prote	813	6	0.8	278	2	D64489	urease accessory p
741	6	0.8	260	2	C95380	conserved hypochet	814	6	0.8	278	2	D75585	hypothetical prote
742	6	0.8	261	2	S53423	major intrinsic pr	815	6	0.8	278	2	B70513	probable lectin 2
743	6	0.8	262	2	S72890	hypothetical prote	816	6	0.8	279	2	T09620	transcription regu
744	6	0.8	262	2	A70577	hypothetical prote	817	6	0.8	279	2	AH1182	nitrate transport
745	6	0.8	263	2	T12407	NADH2 dehydrogenas	818	6	0.8	279	2	F81082	hypothetical prote
746	6	0.8	263	2	G64085	triose-phosphate i	819	6	0.8	279	2	G70807	hypothetical prote
747	6	0.8	263	2	A55279	major intrinsic pr	820	6	0.8	279	2	C75538	hypothetical prote
748	6	0.8	263	2	S73314	hypothetical prote	821	6	0.8	279	2	AI1012	conserved hypochet
749	6	0.8	263	2	I54780	APK1 antigen - hum	822	6	0.8	279	2	A83148	nitrate reductase
750	6	0.8	264	2	B71362	probable exodeoxyr	823	6	0.8	280	2	T07741	maltoextrin ABC t
751	6	0.8	264	2	T10155	hypothetical prote	824	6	0.8	280	2	H95246	glycerol-3-phospha
752	6	0.8	264	2	AI2667	conserved hypochet	825	6	0.8	280	2	A82185	hypothetical prote
753	6	0.8	265	2	D83287	hypothetical prote	826	6	0.8	280	2	T24454	sn-Glycerol-3-phos
754	6	0.8	265	2	A75448	rRNA methylase - D	827	6	0.8	281	1	MMECUE	hypothetical prote
755	6	0.8	265	2	S62363	D-2-chloropropioni	828	6	0.8	281	1	B64227	hypothetical prote
756	6	0.8	266	2	H70858	probable electron	829	6	0.8	281	1	S73813	MG246 homolog H91
757	6	0.8	266	2	S51833	acelin-4 precursor	830	6	0.8	281	2	AI1912	lysophospholipase
758	6	0.8	266	2	C96913	sulfate adenylate	831	6	0.8	281	2	A86012	hypothetical prote
759	6	0.8	266	2	PQ0393	genome polypeptide	832	6	0.8	281	2	A91166	hypothetical prote

833	6	0.8	281	2	C64241	hypothetical prote	906	6	0.8	296	2	F75209	hypothetical prote
834	6	0.8	281	2	T50208	yeast kt112 protei	907	6	0.8	297	2	G87187	phosphoribosylamin
835	6	0.8	281	2	T01445	hypothetical prote	908	6	0.8	297	2	G70708	probable purC prot
836	6	0.8	281	2	F89045	protein B0238.3 [l	909	6	0.8	297	2	A72130	hypothetical prote
837	6	0.8	281	2	AF3407	transporter, dme f	910	6	0.8	297	2	H87613	pilus assembly pro
838	6	0.8	282	2	T06637	hypothetical prote	911	6	0.8	297	2	G95384	probable lytR-fami
839	6	0.8	282	2	A75473	probable sigma fac	912	6	0.8	297	2	AF2980	conserved hypotHet
840	6	0.8	282	2	F82851	conserved hypotHet	913	6	0.8	297	2	H98302	hypothetical prote
841	6	0.8	282	2	D97442	hypothetical prote	914	6	0.8	297	2	I54320	homeobox protein -
842	6	0.8	283	1	I41318	fimbrial adhesin K	915	6	0.8	297	2	A40560	homeotic protein H
843	6	0.8	283	2	T12062	xpEK protein - Xan	916	6	0.8	298	1	G69862	heat-shock protein
844	6	0.8	283	2	D83846	hypothetical prote	917	6	0.8	298	2	S12635	apolipoprotein E p
845	6	0.8	284	2	B46694	conserved hypotHet	918	6	0.8	298	2	D87450	transcription regu
846	6	0.8	284	2	H83119	probable transcrip	919	6	0.8	298	2	I40434	flagellar biosynth
847	6	0.8	284	2	A86604	hypothetical prote	920	6	0.8	298	2	T38937	rna binding protei
848	6	0.8	284	2	T29001	hypothetical prote	921	6	0.8	298	2	T43542	RNA-binding protei
849	6	0.8	284	2	G71192	probable transcrip	922	6	0.8	298	2	F84224	hypothetical prote
850	6	0.8	285	2	A97492	probable cobalt tr	923	6	0.8	298	2	T33220	hypothetical prote
851	6	0.8	285	2	H71938	flagellar motor sw	924	6	0.8	299	2	PN0638	hypothetical prote
852	6	0.8	286	2	AF2829	hydrolase [importe	925	6	0.8	299	2	A99422	hypothetical prote
853	6	0.8	286	2	G69182	thiosulfate sulfur	926	6	0.8	299	2	B70737	permease [importe
854	6	0.8	286	2	H97341	dihydrodipicolinat	927	6	0.8	299	2	S18813	hypothetical prote
855	6	0.8	286	2	A81969	probable chromosom	928	6	0.8	300	2	Ar3101	hypothetical prote
856	6	0.8	287	1	S72569	probable aldehyde	929	6	0.8	300	2	I40215	transcription regu
857	6	0.8	287	2	E98111	hypothetical prote	930	6	0.8	300	2	F75065	hypothetical prote
858	6	0.8	287	2	E82978	conserved hypotHet	931	6	0.8	300	2	H75200	hypothetical prote
859	6	0.8	287	2	T24640	hypothetical prote	932	6	0.8	300	2	D71234	hypothetical prote
860	6	0.8	287	2	F64648	flly protein - Hel	933	6	0.8	300	2	AF2846	permease [importe
861	6	0.8	287	2	AE3578	glycine betaine/l-	934	6	0.8	300	2	F97623	hypothetical prote
862	6	0.8	288	2	E83946	pyruvate synthase	935	6	0.8	301	2	C69837	5-oxo-l,2,5-tricar
863	6	0.8	288	2	C56281	7alpha-cephe-meth	936	6	0.8	301	2	S50737	probable membrane
864	6	0.8	288	2	S18438	sporulation protei	937	6	0.8	301	2	C96961	cell division prot
865	6	0.8	288	2	AB0291	probable exported	938	6	0.8	302	1	WZBE9	gene 9 protein - h
866	6	0.8	288	2	JS0659	homeotic protein H	939	6	0.8	302	2	T40490	probable 26S prote
867	6	0.8	289	1	S35294	probable glucose-1	940	6	0.8	302	2	F81016	conserved hypotHet
868	6	0.8	289	1	S55649	deoxyuridine triph	941	6	0.8	302	2	F90158	DNA repair endo/ex
869	6	0.8	289	2	A95158	homoserine kinase	942	6	0.8	302	2	H87476	conserved hypotHet
870	6	0.8	289	2	A98024	homoserine kinase	943	6	0.8	302	2	B82968	probable transcrip
871	6	0.8	289	2	AB0262	conserved hypotHet	944	6	0.8	302	2	S75481	probable chemotaxi
872	6	0.8	289	2	H86522	CT144 hypothetical	945	6	0.8	303	2	AC0092	ADP-ribosyl cyclas
873	6	0.8	289	2	B72099	conserved hypotHet	946	6	0.8	303	2	JC2410	hypothetical prote
874	6	0.8	289	2	C71501	probable outer mem	947	6	0.8	303	2	F71680	conserved hypotHet
875	6	0.8	289	2	B85794	hypothetical prote	948	6	0.8	303	2	H81818	hypothetical prote
876	6	0.8	289	2	S75197	ABC-type transport	949	6	0.8	303	2	S75557	probable AraC-type
877	6	0.8	290	1	KIRPAS	phosphoribulokinas	950	6	0.8	303	2	B47089	probable permease
878	6	0.8	290	2	A86038	involved in lipopo	951	6	0.8	303	2	B96909	hypothetical prote
879	6	0.8	290	2	H91190	hypothetical prote	952	6	0.8	303	2	G71166	conserved hypotHet
880	6	0.8	290	2	S47839	short-chain dehydr	953	6	0.8	304	1	B69449	pyridoxine biosynt
881	6	0.8	291	2	AH3074	probable short-cha	954	6	0.8	304	2	T46647	ribonucleoside-dip
882	6	0.8	291	2	A96212	conserved hypotHet	955	6	0.8	305	2	T03155	acylttransferase (E
883	6	0.8	291	2	A81659	phosphoribulokinas	956	6	0.8	305	2	AB2494	mrr restriction sy
884	6	0.8	292	1	B35819	probable membrane	957	6	0.8	305	2	AD2494	hypothetical prote
885	6	0.8	292	2	D97199	hypothetical prote	958	6	0.8	305	2	H75091	phosphoribosylamin
886	6	0.8	292	2	S23239	hypothetical prote	959	6	0.8	306	2	E64138	phosomosal protein
887	6	0.8	293	1	D69300	4-hydroxybenzoate	960	6	0.8	306	2	A89952	inosine-uridine pr
888	6	0.8	293	2	A89818	hypothetical prote	961	6	0.8	306	2	AE3100	inosine-uridine pr
889	6	0.8	293	2	AH1095	conserved hypotHet	962	6	0.8	306	2	E38186	transcriptional re
890	6	0.8	293	2	JN0651	rRNA methyltransfe	963	6	0.8	306	2	AF3230	probable ABC-type
891	6	0.8	293	2	B75441	conserved hypotHet	964	6	0.8	307	2	T36764	cysteine synthase
892	6	0.8	293	2	T32229	hypothetical prote	965	6	0.8	307	2	H83660	primosome componen
893	6	0.8	293	2	A97313	transcription regu	966	6	0.8	307	2	AH1269	primosome componen
894	6	0.8	293	2	AH0143	probable membrane	967	6	0.8	307	2	AB1632	hypothetical prote
895	6	0.8	294	1	KFMS3	tissue factor prec	968	6	0.8	307	2	S30432	Na+/Ca2+ exchangin
896	6	0.8	294	2	T11379	NADH2 dehydrogenas	969	6	0.8	307	2	G90270	conserved hypotHet
897	6	0.8	294	2	T35492	probable endonucle	970	6	0.8	307	2	G69211	hypothetical prote
898	6	0.8	294	2	B81427	H+-transporting tw	971	6	0.8	307	2	T24423	ferrochelatase (EC
899	6	0.8	294	2	G97449	hypothetical prote	972	6	0.8	308	2	S70735	conserved hypotHet
900	6	0.8	295	2	F69976	conserved hypotHet	973	6	0.8	308	2	D69348	hypothetical prote
901	6	0.8	295	2	H99713	30S ribosomal prot	974	6	0.8	308	2	A99993	tropinesterase (at
902	6	0.8	295	2	A60131	homeotic protein X	975	6	0.8	309	2	D97607	dihydrodipicolinat
903	6	0.8	296	2	D75597	glucose-1-phosphat	976	6	0.8	309	2	D64752	probable epimerase
904	6	0.8	296	2	E71717	ribosomal protein	977	6	0.8	309	2	C83136	
905	6	0.8	296	2	S39746	hypothetical prote	978	6	0.8	309	2		

979	6	0.8	309	2	F97168	nucleoside-diphosp
980	6	0.8	309	2	G85988	probable transcrip
981	6	0.8	309	2	E65116	hypothetical prote
982	6	0.8	309	2	D91143	probable transcrip
983	6	0.8	309	2	T20518	hypothetical prote
984	6	0.8	309	2	T38671	Zinc finger, C3HC4
985	6	0.8	310	2	C47045	ferrochelatase (EC
986	6	0.8	310	2	A12654	glycyl-tRNA synthe
987	6	0.8	310	2	S45130	autophagocytosis p
988	6	0.8	310	2	H82439	hypothetical prote
989	6	0.8	310	2	AG1733	gp49 (Bacteriophag
990	6	0.8	310	2	B75476	conserved hypothet
991	6	0.8	310	2	G94809	hypothetical prote
992	6	0.8	311	2	I64082	pantothenate kinase
993	6	0.8	311	2	T11532	phosphoribosylamin
994	6	0.8	311	2	G75121	nucleolar protein
995	6	0.8	311	2	F95349	hypothetical prote
996	6	0.8	311	2	H75411	conserved hypothet
997	6	0.8	311	2	A83329	probable phosphati
998	6	0.8	311	2	E70539	hypothetical prote
999	6	0.8	312	1	S46047	probable 3-methyl-
1000	6	0.8	312	2	T08076	adenyl-yl-sulfate k
ALIGNMENTS						
RESULT 1						
outer membrane protein OMP85 NMA0085 [imported] - Neisseria meningitidis (strain Z2491)						
C;Species: Neisseria meningitidis						
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004						
C;Accession: D82000						
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel						
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,						
Nature 404, 502-506, 2000						
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.						
A;Reference number: A81775; MUID:20222556; PMID:10761919						
A;Accession: D82000						
A;Status: preliminary						
A;Molecule type: DNA						
A;Residues: 1-797 <PAR>						
A;Cross-references: UNIPROT:Q9JX31; UNIPARC:UPI0000003C425; GB:AL162752; GB:AL157959; NID						
A;Experimental source: serogroup A, strain Z2491						
C;Genetics:						
A;Gene: Omp85; NMA0085						
C;Superfamily: protective surface antigen D-15						
Query Match 94.4%; Score 752; DB 2; Length 797;						
Best Local Similarity 100.0%; Pred. No. 0;						
Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
Qy	21	ADFTIQDIRVEGLQRTPESTVFNYPVKVGDTYNDTHGSAIIKSLYATGFFDDVRVETAD 80				
Db	21	ADFTIQDIRVEGLQRTPESTVFNYPVKVGDTYNDTHGSAIIKSLYATGFFDDVRVETAD 80				
Qy	81	GQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSQYFNQATLNOAVAGLKEEY 140				
Db	81	GQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSQYFNQATLNOAVAGLKEEY 140				
Qy	141	LGRGKLNITQTPKVTKLARNRVDITIDEGSKAKITDIEFEGNQVYSDRKLQRMSLTE 200				
Db	141	LGRGKLNITQTPKVTKLARNRVDITIDEGSKAKITDIEFEGNQVYSDRKLQRMSLTE 200				
Qy	201	GGIWTWLTNRNQNEOKFAQDMKVTFYNNQYGFDFRILDTDTQTNEDTKQTIKITVH 260				
Db	201	GGIWTWLTNRNQNEOKFAQDMKVTFYNNQYGFDFRILDTDTQTNEDTKQTIKITVH 260				
Qy	261	EGGRFRWGVKVSIEGDTNEVPKAELEKLLTMKPGKMYERQQTAVLGEIQNRMSGAGVAYS 320				
Db	261	EGGRFRWGVKVSIEGDTNEVPKAELEKLLTMKPGKMYERQQTAVLGEIQNRMSGAGVAYS 320				
Qy	321	EISVQPLPNAETKTVDVFLHIEPGRKIYNEIHITGNKTRDEVVRELQMESAPYDTS 380				

Db	321	EISVQPLPNAETKTVDVFLHIEPGRKIYNEIHITGNKTRDEVVRELQMESAPYDTS 380				
Qy	381	KLQRSKERVLLGYPFNQVQFDVPLAGTDPKVDLNNSLTERSTGSLDLGAGWVQDTGLVM 440				
Db	381	KLQRSKERVLLGYPFNQVQFDVPLAGTDPKVDLNNSLTERSTGSLDLGAGWVQDTGLVM 440				
Qy	441	SAGVSQDNLFQGTCKSAALRASRSKTTLNGSLSTDPYFTADGYSGLGVYDVYKAPDRKAS 500				
Db	441	SAGVSQDNLFQGTCKSAALRASRSKTTLNGSLSTDPYFTADGYSGLGVYDVYKAPDRKAS 500				
Qy	501	TSIQKQVKTITAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHADFIKKYKGTG 560				
Db	501	TSIQKQVKTITAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHADFIKKYKGTG 560				
Qy	561	TGGSFPGWLYKGTVGWRNKTDLSALWPTRGYLTGVNAEIALPGSLQYVSATHNQWTFPP 620				
Db	561	TGGSFPGWLYKGTVGWRNKTDLSALWPTRGYLTGVNAEIALPGSLQYVSATHNQWTFPP 620				
Qy	621	LSKTFTMLGGEVGIAGGYGRTKEIPFFENFYGGGLGSVRGYESGTLGPKVYDEYGEKIS 680				
Db	621	LSKTFTMLGGEVGIAGGYGRTKEIPFFENFYGGGLGSVRGYESGTLGPKVYDEYGEKIS 680				
Qy	681	YGGNKKANYSAEELFFPMGAKDARTVRLSLFADAGSVWDGKTYDDNSSSATGGRVQNIY 740				
Db	681	YGGNKKANYSAEELFFPMGAKDARTVRLSLFADAGSVWDGKTYDDNSSSATGGRVQNIY 740				
Qy	741	AGNTHKSTFTNELRYSAGGAVTWLSPGPMKF 772				
Db	741	AGNTHKSTFTNELRYSAGGAVTWLSPGPMKF 772				
RESULT 2						
G81228						
outer membrane protein Omp85 NMB0182 [imported] - Neisseria meningitidis (strain MC58)						
C;Species: Neisseria meningitidis						
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004						
C;Accession: G81228						
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.						
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;						
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.						
Science 287, 1809-1815, 2000						
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver						
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.						
A;Reference number: A81000; MUID:20175755; PMID:10710307						
A;Accession: G81228						
A;Status: preliminary						
A;Molecule type: DNA						
A;Residues: 1-797 <TET>						
A;Cross-references: UNIPROT:Q9K1H0; UNIPARC:UPI0000003C41F; GB:AE002375; GB:AE002098; NID						
A;Experimental source: serogroup B, strain MC58						
C;Genetics:						
A;Gene: NMB0182						
C;Superfamily: protective surface antigen D-15						
Query Match 94.4%; Score 752; DB 2; Length 797;						
Best Local Similarity 100.0%; Pred. No. 0;						
Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
Qy	21	ADFTIQDIRVEGLQRTPESTVFNYPVKVGDTYNDTHGSAIIKSLYATGFFDDVRVETAD 80				
Db	21	ADFTIQDIRVEGLQRTPESTVFNYPVKVGDTYNDTHGSAIIKSLYATGFFDDVRVETAD 80				
Qy	81	GQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSQYFNQATLNOAVAGLKEEY 140				
Db	81	GQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSQYFNQATLNOAVAGLKEEY 140				
Qy	141	LGRGKLNITQTPKVTKLARNRVDITIDEGSKAKITDIEFEGNQVYSDRKLQRMSLTE 200				
Db	141	LGRGKLNITQTPKVTKLARNRVDITIDEGSKAKITDIEFEGNQVYSDRKLQRMSLTE 200				
Qy	201	GGIWTWLTNRNQNEOKFAQDMKVTFYNNQYGFDFRILDTDTQTNEDTKQTIKITVH 260				
Db	201	GGIWTWLTNRNQNEOKFAQDMKVTFYNNQYGFDFRILDTDTQTNEDTKQTIKITVH 260				
Qy	261	EGGRFRWGVKVSIEGDTNEVPKAELEKLLTMKPGKMYERQQTAVLGEIQNRMSGAGVAYS 320				
Db	261	EGGRFRWGVKVSIEGDTNEVPKAELEKLLTMKPGKMYERQQTAVLGEIQNRMSGAGVAYS 320				
Qy	321	EISVQPLPNAETKTVDVFLHIEPGRKIYNEIHITGNKTRDEVVRELQMESAPYDTS 380				

Db 201 GGIWTLTRSNQFNEQFAQDMKVTDFYQNNGYDFRLLDITDQTNEDKTKQTIKIVH 260  
Qy 261 EGGRFRWGVKSIEGDTNVPKAELEKLLTMKPKWYERQOMTAVLGEIQNRMGSGAGVAYS 320  
Db 261 EGGRFRWGVKSIEGDTNVPKAELEKLLTMKPKWYERQOMTAVLGEIQNRMGSGAGVAYS 320  
Qy 321 EISVQPLNAETKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVVRRRELROMESAPYDTS 380  
Db 321 EISVQPLNAETKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVVRRRELROMESAPYDTS 380  
Qy 381 KLORSKERVLLGYFDNVQFOFADVPLAGTDPKVDLNNLSLTERSTGSLDLSAGWQDTGLVM 440  
Db 381 KLORSKERVLLGYFDNVQFOFADVPLAGTDPKVDLNNLSLTERSTGSLDLSAGWQDTGLVM 440  
Qy 441 SAGVSQDNLFGTGKSAALRAGRSKTTLNGSLSFDPYPTADGVSLGYVYVYKAFDPPRKAS 500  
Db 441 SAGVSQDNLFGTGKSAALRAGRSKTTLNGSLSFDPYPTADGVSLGYVYVYKAFDPPRKAS 500  
Qy 501 TSIKQYKTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHVADFKKYGKTDG 560  
Db 501 TSIKQYKTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHVADFKKYGKTDG 560  
Qy 561 TDGSPFKWLYKGTGCGRNKTDLSALWPTRGYLTGVNAELALPGSKLOYYSATHNOTWFFP 620  
Db 561 TDGSPFKWLYKGTGCGRNKTDLSALWPTRGYLTGVNAELALPGSKLOYYSATHNOTWFFP 620  
Qy 621 LSKTFTMLGSGVGIAGGYGRKTEIPFPENFYGGGLGSGVRGYESGTLGPKVYDEYGEKIS 680  
Db 621 LSKTFTMLGSGVGIAGGYGRKTEIPFPENFYGGGLGSGVRGYESGTLGPKVYDEYGEKIS 680  
Qy 681 YGCKKANKVSAELLFPMPCAKADARTVRLSLFADAGSVMDGKTYDDNSSATGGRVQNIYG 740  
Db 681 YGCKKANKVSAELLFPMPCAKADARTVRLSLFADAGSVMDGKTYDDNSSATGGRVQNIYG 740  
Qy 741 AGNTHKSTFTNELRYSAGGAVTWLSPLGPMKF 772  
Db 741 AGNTHKSTFTNELRYSAGGAVTWLSPLGPMKF 772

RESULT 3  
T46206  
hypothetical protein T8P19\_130 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 09-Jul-2004  
C:Accession: T46206  
R:Choisne, N.; Robert, C.; Bröttier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; Sa  
submitted to the Protein Sequence Database, December 1999  
A:Reference number: 223008  
A:Accession: T46206  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-328 <CHO>  
A:Cross-references: UNIPROT:Q9SMN7; UNIPARC:UPI000000A5A5F; EMBL:AL133315  
A:Experimental source: cultivar Columbia; BAC clone T8P19  
C:Genetics:  
A:Map position: 3  
A:Introns: 39/2; 62/3; 94/3; 133/2; 179/3; 277/1  
A:Note: T8P19\_130

Query Match 1.1%; Score 9; DB 2; Length 328;  
Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 654 GGLGSGVRGY 662  
Db 152 GGLGSGVRGY 160

RESULT 4  
T49132  
hypothetical protein F26G5.110 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 09-Jul-2004

C:Accession: T49132  
R:D'Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Rudd, S.; Le  
submitted to the Protein Sequence Database, April 2000  
A:Reference number: 225017  
A:Accession: T49132  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-435 <DAN>  
A:Cross-references: UNIPROT:Q9LXP7; UNIPARC:UPI000000A38BD; EMBL:AL353814; GSPDB:GN00061;  
A:Experimental source: cultivar Columbia; BAC clone F26G5  
C:Genetics:  
A:Gene: ATSP:F26G5.110  
A:Map position: 3  
A:Introns: 12/1; 34/2; 135/3; 188/3; 212/2; 238/3; 277/2; 326/3; 350/1; 395/1

Query Match 1.1%; Score 9; DB 2; Length 435;  
Best Local Similarity 100.0%; Pred. No. 1.5;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 654 GGLGSGVRGY 662  
Db 296 GGLGSGVRGY 304

RESULT 5  
A96984  
hypothetical protein CAC0683 [imported] - Clostridium acetobutylicum  
C:Species: Clostridium acetobutylicum  
C:Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004  
C:Accession: A96984  
R:Nolling, J.; Breston, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,  
; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4836, 2001  
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo  
A:Reference number: A96900; MUID:21359325; PMID:21359325  
A:Accession: A96984  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-129 <KUR>  
A:Cross-references: UNIPROT:Q97L79; UNIPARC:UPI000000C9F47; GB:AE001437; PIDN:AAK78660.1;  
A:Experimental source: Clostridium acetobutylicum ATCC824  
C:Genetics:  
A:Gene: CAC0683

Query Match 1.0%; Score 8; DB 2; Length 129;  
Best Local Similarity 100.0%; Pred. No. 5.7;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 670 KVDYDEYGE 677  
Db 17 KVDYDEYGE 24

RESULT 6  
E84423  
hypothetical protein At2G01340 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C:Accession: E84423  
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, J.  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-769, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487; PMID:10617197  
A:Accession: E84423  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-225 <STO>  
A:Cross-references: UNIPROT:Q9ZU33; UNIPARC:UPI000000A4EBB; GB:AE002093; NID:G4262241; P  
C:Genetics:  
A:Gene: At2G01340  
A:Map position: 2

```
Query Match 1.0%; Score 8; DB 2; Length 225;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 280 PKAELEKL 287
Db 144 PKAELEKL 151

RESULT 7
glycerate dehydrogenase PAB2374 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 05-Oct-2004
C:Accession: B75057
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A:Reference number: A75001
A:Accession: B75057
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-335 <KAW>
A:Cross-references: UNIPROT:Q9UVRL; UNIPARC:UPI0000034704; GB:AJ248287; GB:AL096836; NID
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: gdh-like; PAB2374
C:Superfamily: Phosphoglycerate dehydrogenase

Query Match 1.0%; Score 8; DB 2; Length 335;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 485 LGYDVYVK 492
Db 145 LGYDVYVK 152

RESULT 8
formate dehydrogenase accessory protein VC1519 [imported] - Vibrio cholerae (strain N169
C:Species: Vibrio cholerae
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: C82190
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: C82190
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-337 <HEL>
A:Cross-references: UNIPROT:Q9KRW5; UNIPARC:UPI00000C2FF4; GB:AE004230; GB:AE003852; NID
A:Experimental source: serogroup O1; strain N16961; biotype E1 Tor
C:Genetics:
A:Gene: VC1519
A:Map position: 1
C:Superfamily: formate dehydrogenase accessory protein FdhD

Query Match 1.0%; Score 8; DB 2; Length 337;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 671 VYDEYGEK 678
Db 81 VYDEYGEK 88

RESULT 9
A71175
```

```
probable dehydrogenase - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C>Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 31-Dec-2004
C:Accession: A71175
R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekine
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushiida, N.; Oguchi,
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic ar
A:Reference number: A71000; MUID:98344137; PMID:9679194
A:Accession: A71175
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-376 <KAW>
A:Cross-references: UNIPROT:O58320; UNIPARC:UPI00000667E3; GB:AF000002; NID:G3236129; PFI
A:Experimental source: strain OT3
A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
C:Genetics:
A:Gene: PH0597
C:Superfamily: D-3-phosphoglycerate dehydrogenase with ACT domain

Query Match 1.0%; Score 8; DB 2; Length 376;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 485 LGYDVYVK 492
Db 186 LGYDVYVK 193

RESULT 10
T04985
probable transaminase [EC 2.6.1.-] T16L1.170 [similarity] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T04985
R;Bevan, M.; Obermaier, B.; Deutschenbaur, S.; Piravandi, E.; Hoheisel, J.; Mewes, H.W.;
submitted to the Protein Sequence Database, November 1998
A:Reference number: Z15393
A:Accession: T04985
A:Molecule type: DNA
A:Residues: 1-426 <BEV>
A:Cross-references: UNIPROT:O81885; UNIPARC:UPI0000048A52; EMBL:AL031394
A:Experimental source: cultivar Columbia; BAC clone T16L1
C:Genetics:
A:Map position: 4
A:Introns: 19/1; 41/3; 80/3; 101/3; 136/3; 153/3; 260/3; 329/3
A:Note: T16L1.170
C:Superfamily: aspartate transaminase
C:Keywords: aminotransferase

Query Match 1.0%; Score 8; DB 2; Length 426;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 484 SLGYDVYVG 491
Db 351 SLGYDVYVG 358

RESULT 11
G42365
flagellar hook-length control protein fliK - Bacillus subtilis
N:Alternate names: hypothetical protein 7 (flaA operon)
C:Species: Bacillus subtilis
C>Date: 24-Jul-1992 #sequence_revision 24-Jul-1992 #text_change 09-Jul-2004
C:Accession: G42365; G69624; S14500
R;Albertini, A.M.; Caramori, T.; Crabb, W.D.; Scoffone, F.; Galizzi, A.
J. Bacteriol. 173, 3573-3579, 1991
A:Title: The flaA locus of Bacillus subtilis is part of a large operon coding for flagell
A:Reference number: A42365; MUID:91258343; PMID:1828465
A:Accession: G42365
A:Molecule type: DNA
A:Residues: 1-429 <ALB>
```

A;Cross-references: UNIPROT:P23451; UNIPARC:UPI00000603E2; EMBL:X56049; NID:G39904; PIDN:R;Kunst, F.; Ogawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter, C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho, A.; Ehrlich, S.D.; Emmerson, P.F.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallen, Iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koeter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Maueel, P.; Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A;Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seron, akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terptrata, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yanane, K.; Yasumoto, K.; Yata, K.; Yoshida, K. A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A. Bacillus subtilis. A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A;Reference number: A69580; MUID:98044033; PMID:9384377

A;Accession: G69624

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-429 <KUN>

A;Cross-references: UNIPARC:UPI00000603E2; GB:Z99112; GB:AL009126; NID:G2633902; PIDN:CA

A;Experimental source: strain 168

C;Genetics:

A;Gene: flik

Query Match 1.0%; Score 8; DB 2; Length 429;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 328 PNAETKV 335  
|||||||

Db 286 PNAETKV 293

RESULT 12

IMBP4

site-specific recombinase for integration and excision - Bacillus phage phi-105

N;Alternate names: immunity region protein 3, 4, 5, 6

C;Species: Bacillus phage phi-105

C;Date: 31-Dec-1988 #sequence revision 22-Oct-1999 #text\_change 09-Jul-2004

C;Accession: T13541; D24521; D24521; F24521

R;Kobayashi, K.; Okamura, K.; Inoue, T.; Sato, T.; Kobayashi, Y. submitted to the EMBL Data Library, July 1998

A;Description: Complete nucleotide sequence of Bacillus subtilis phage phi-105.

A;Reference number: Z17688

A;Accession: T13541

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-474 <KOB>

A;Cross-references: UNIPROT:Q9T200; UNIPARC:UPI000009B54B; EMBL:AB016282; PIDN:BAA36658.

R;Cully, D.F.; Garro, A.J. Gene 38, 153-164, 1985

A;Title: Nucleotide sequence of the immunity region of Bacillus subtilis bacteriophage B

A;Reference number: A91535; MUID:86056972; PMID:3934047

A;Accession: C24521

A;Molecule type: DNA

A;Residues: 1-78, 'MTHC' <CUL>

A;Cross-references: UNIPARC:UPI000013B43C; GB:M11920; NID:G215477; PIDN:AAA88399.1; PID:

A;Accession: D24521

A;Molecule type: DNA

A;Residues: 149-160, 'AR', '163', 'H', 'HSDSQRRVR', '381-383', 'RIQRARS', '392 <CU2>

A;Cross-references: UNIPARC:UPI000013B43D; GB:M11920; NID:G215477; PIDN:AAA88401.1; PID:

A;Accession: E24521

A;Molecule type: DNA

A;Residues: 189-318, 'HAP', <CU3>

A;Cross-references: UNIPARC:UPI0000174BB8; GB:M11920

A;Accession: F24521

A;Molecule type: DNA

A;Residues: 'MP', '319-376', 'RNTK', '381', 'PGPWS', <CU4>

A;Cross-references: UNIPARC:UPI0000174BB9; GB:M11920

C;Superfamily: phage phi-105 site-specific recombinase

C;Keywords: early protein

Query Match 1.0%; Score 8; DB 1; Length 474;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 168 IDEGKSAK 175  
|||||||

Db 53 IDEGKSAK 60

## RESULT 13

G83375

probable glycosyl hydrolase PA2164 [imported] - Pseudomonas aeruginosa (strain PA01)

C;Species: Pseudomonas aeruginosa

C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004

C;Accession: G83375

R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br

adman, S.; Yuan, Y.; Brody, L.B.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,

; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000

A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho

A;Reference number: A82950; MUID:20437337; PMID:10984043

A;Accession: G83375

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-583 <STO>

A;Cross-references: UNIPROT:Q9I1V1; UNIPARC:UPI000000C55E1; GB:AE004643; GB:AE004091; NID

A;Experimental source: strain PA01

C;Genetics:

A;Gene: PA2164

C;Superfamily: glycosyltrehalose trehalohydrolase

Query Match 1.0%; Score 8; DB 2; Length 583;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 74 VRVETADG 81  
|||||||

Db 29 VRVETADG 36

## RESULT 14

JE0327

dynamin-related protein MSPI - fission yeast (Schizosaccharomyces pombe)

C;Species: Schizosaccharomyces pombe

C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004

C;Accession: JE0327

R;Pellouquin, L.; Belenguer, P.; Menon, Y.; Ducommun, B.

Biochem. Biophys. Res. Commun. 251, 720-726, 1998

A;Title: Identification of a fission yeast dynamin-related protein involved in mitochond

A;Reference number: JE0327; MUID:99008891; PMID:9790976

A;Accession: JE0327

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-903 <PEL>

A;Cross-references: UNIPROT:P87320; UNIPARC:UPI0000169165; GB:Y07891; NID:G2231081; PIDN

C;Genetics:

A;Gene: MSPI

Query Match 1.0%; Score 8; DB 2; Length 903;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 455 SAALRASR 462  
|||||||

Db 417 SAALRASR 424

## RESULT 15

TS0334

dynamin-related protein [imported] - fission yeast (Schizosaccharomyces pombe)

C;Species: Schizosaccharomyces pombe

C;Date: 09-Jun-2000 #sequence\_revision 09-Jun-2000 #text\_change 09-Jul-2004

C;Accession: T50334  
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Brown, S.; Harris, D.  
submitted to the EMBL Data Library, February 2000  
A;Reference number: Z25062  
A;Accession: T50334  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-903 <LYN>  
A;Cross-references: UNIPROT:P87320; UNIPARC:UPI000012F637; EMBL:AL157874; PIDN:CAB75996.  
A;Experimental source: strain 972h(-); cosmid c1718  
C;Genetics:  
A;Gene: SPDB:SPBC1718.06  
A;Map position: 2

Query Match 1.0%; Score 8; DB 2; Length 903;  
Best Local Similarity 100.0%; Pred.No. 32;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 455 SAALRASR 462  
Db 417 SAALRASR 424

Search completed: April 12, 2006, 16:23:44  
Job time : 67 secs



GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: April 12, 2006, 16:14:58 ; Search time 190 Seconds  
(without alignments)  
1843.078 Million cell updates/sec

Title: US-10-606-618-4  
Perfect score: 797  
Sequence: 1 MKLQIASALMLGISPLAF.....LKKPEDEIQRFQLGTTF 797

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2441997

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : A\_Geneseq\_21:\*

1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	797	100.0	797	3	AAY84947 Amino aci
2	797	100.0	797	5	ABY79802 Neisseria
3	797	100.0	797	9	ADZ09417 Neisseria
4	752	94.4	797	4	AU03959 Neisseria
5	752	94.4	797	4	AU03957 Neisseria
6	752	94.4	797	4	AU04451 Neisseria
7	752	94.4	797	4	AU04451 Neisseria
8	752	94.4	797	4	AU04451 Neisseria
9	752	94.4	797	4	AU04451 Neisseria
10	752	94.4	797	4	AU04451 Neisseria
11	752	94.4	797	4	AU04451 Neisseria
12	210	26.3	792	4	AU03958 Neisseria
13	210	26.3	792	4	AU03958 Neisseria
14	210	26.3	792	4	AU03958 Neisseria
15	210	26.3	792	6	ABP80499 N. gonorr
16	210	26.3	792	6	ABP80499 N. gonorr
17	157	19.7	792	3	ABY79748 Amino aci
18	157	19.7	792	3	ABY79748 Amino aci
19	157	19.7	792	5	ABG91064 Neisseria
20	157	19.7	792	5	ABG91064 Neisseria
21	37	4.6	37	4	AU04410 Neisseria
22	32	4.0	32	4	AU04410 Neisseria
23	29	3.6	29	4	AU03987 Neisseria
24	25	3.1	25	4	AU04412 Neisseria

25	3.1	25	4	AAU04000	Aau04000 Neisseria
26	2.9	23	4	AAU03971	Aau03971 Neisseria
27	2.8	22	4	AAU04401	Aau04401 Neisseria
28	2.6	21	4	ABY23787	Abz23787 Neisseria
29	2.4	19	4	AAU03988	Aau03988 Neisseria
30	2.4	21	4	AAU03985	Abz3785 Neisseria
31	2.4	21	4	AAU04428	Aau04428 Neisseria
32	2.3	18	4	AAU04434	Aau04434 Neisseria
33	2.3	18	4	AAU04425	Aau04425 Neisseria
34	2.3	18	4	AAU03990	Aau03990 Neisseria
35	2.0	16	4	AAU04427	Aau04427 Neisseria
36	2.0	16	4	AAU04435	Aau04435 Neisseria
37	2.0	16	4	AAU03992	Aau03992 Neisseria
38	2.0	16	4	AAU04430	Aau04430 Neisseria
39	1.9	15	4	AAU04442	Aau04442 Neisseria
40	1.9	15	4	AAU04404	Aau04404 Neisseria
41	1.9	15	4	ABY84743	Abz84743 N-termina
42	1.8	14	4	AAU04438	Aau04438 Neisseria
43	1.8	14	4	AAU03980	Aau03980 Neisseria
44	1.8	14	4	AAU03984	Aau03984 Neisseria
45	1.6	13	4	AAU03985	Aau03985 Neisseria
46	1.5	12	4	AAU04423	Aau04423 Neisseria
47	1.5	12	4	AAU04424	Aau04424 Neisseria
48	1.5	12	4	AAU04416	Aau04416 Neisseria
49	1.5	12	4	AAU04418	Aau04418 Neisseria
50	1.5	12	4	AAU03986	Aau03986 Neisseria
51	1.4	11	4	AAU03981	Aau03981 Neisseria
52	1.4	11	4	AAU03999	Aau03999 Neisseria
53	1.4	11	4	ABY23789	Abz23789 Neisseria
54	1.3	10	4	AAU03993	Aau03993 Neisseria
55	1.3	10	4	AAU03982	Aau03982 Neisseria
56	1.3	10	4	AAU03975	Aau03975 Neisseria
57	1.3	10	4	AAU04413	Aau04413 Neisseria
58	1.3	10	4	AAU03974	Aau03974 Neisseria
59	1.3	10	4	AAU04411	Aau04411 Neisseria
60	1.3	10	4	AAU04450	Aau04450 Neisseria
61	1.3	10	4	AAU04405	Aau04405 Neisseria
62	1.3	10	4	AAU04408	Aau04408 Neisseria
63	1.3	10	4	AAU04439	Aau04439 Neisseria
64	1.3	10	4	AAU04403	Aau04403 Neisseria
65	1.3	10	4	AAU03965	Aau03965 Neisseria
66	1.1	9	4	AAU04448	Aau04448 Neisseria
67	1.1	9	4	AAU03961	Aau03961 Neisseria
68	1.1	9	4	AAU04414	Aau04414 Neisseria
69	1.1	9	4	AAU03994	Aau03994 Neisseria
70	1.1	9	4	AAU03967	Aau03967 Neisseria
71	1.1	9	4	AAU04420	Aau04420 Neisseria
72	1.1	9	4	AAU03995	Aau03995 Neisseria
73	1.1	9	4	AAU03991	Aau03991 Neisseria
74	1.1	9	4	AAU03998	Aau03998 Neisseria
75	1.1	9	4	AAU04447	Aau04447 Neisseria
76	1.1	12	4	AAU03964	Aau03964 Neisseria
77	1.1	177	8	ADY07476	Ady07476 Plant ful
78	1.1	185	3	AAU03957	AAU03957 Neisseria
79	1.1	334	3	AAU03957	AAU03957 Neisseria
80	1.1	362	3	AAU03957	AAU03957 Neisseria
81	1.1	408	6	ADY24586	Ady24586 Plant ful
82	1.1	798	8	ABM67563	Abm67563 Photorhab
83	1.1	1035	8	ADJ50326	Adj50326 Oil-assoc
84	1.0	8	4	AAU04436	Aau04436 Neisseria
85	1.0	8	4	AAU03996	Aau03996 Neisseria
86	1.0	8	4	AAU04422	Aau04422 Neisseria
87	1.0	8	4	AAU04445	Aau04445 Neisseria
88	1.0	8	4	AAU04402	Aau04402 Neisseria
89	1.0	8	4	AAU04426	Aau04426 Neisseria
90	1.0	8	4	AAU03970	Aau03970 Neisseria
91	1.0	8	4	AAU03973	Aau03973 Neisseria
92	1.0	8	4	AAU03977	Aau03977 Neisseria
93	1.0	94	7	ABO61646	Abz61646 Klebsiell
94	1.0	95	3	ABG25177	Abz25177 Arabidops
95	1.0	97	4	ABY51139	Abz51139 Human sec
96	1.0	97	6	ABO45396	Abz45396 Novel hum
97	1.0	97	7	ABO26876	Abz26876 Protein a

98	8	1.0	116	3	AAG57649	Aag57649	Arabidops	171	7	0.9	83	4	AAU60561	Aau60561	Proptonib
99	8	1.0	117	3	AAG49893	Aag49893	Arabidops	172	7	0.9	83	6	ABM57080	Abm57080	Proptonib
100	8	1.0	126	3	AAG25176	Aag25176	Arabidops	173	7	0.9	85	8	ADS42710	Adas42710	Bacterial
101	8	1.0	201	3	AAG57648	Aag57648	Arabidops	174	7	0.9	86	6	ADA34965	Ada34965	Aginetoba
102	8	1.0	202	3	AAG49892	Aag49892	Arabidops	175	7	0.9	86	7	ABO63968	Abog63968	Klebsiell
103	8	1.0	214	3	AAG57647	Aag57647	Arabidops	176	7	0.9	87	4	AAU17729	Aau17729	Novel hum
104	8	1.0	215	3	AAG49891	Aag49891	Arabidops	177	7	0.9	87	7	ADG41109	Adga41109	Human res
105	8	1.0	216	5	ADN21670	Adn21670	Bacterial	178	7	0.9	87	7	AD196883	Adi96883	Human res
106	8	1.0	217	5	ABG60322	Abg60322	Yeast dyn	179	7	0.9	88	3	AAV86404	Aay86404	Human gen
107	8	1.0	250	8	ADX88498	Adx88498	Plant ful	180	7	0.9	88	6	ABO53551	Abos3551	Novel hum
108	8	1.0	266	4	ABG15869	Abg15869	Novel hum	181	7	0.9	92	7	ADE08224	Ade08224	Novel pro
109	8	1.0	266	7	ADC32990	Adc32990	Human nov	182	7	0.9	96	4	AAU64929	Aau64929	Proptonib
110	8	1.0	274	9	ABM96353	Abm96353	M. xanthu	183	7	0.9	96	6	ABM61448	Abm61448	Proptonib
111	8	1.0	289	3	AAG49003	Aag49003	Arabidops	184	7	0.9	97	7	ABO69614	Abog69614	Pseudomon
112	8	1.0	299	4	AAG90486	Aag90486	C glutami	185	7	0.9	101	4	ABB17344	Abb17344	Human ner
113	8	1.0	315	8	ADS24860	Ads24860	Bacterial	186	7	0.9	102	7	ADM27054	Adm27054	Hyperther
114	8	1.0	321	8	ADU02334	Adu02334	Novel hum	187	7	0.9	110	3	AAG02520	Aag02520	Human sec
115	8	1.0	335	4	AAU96813	Aau96813	Putative	188	7	0.9	110	4	AAO06467	Aao06467	Human pol
116	8	1.0	336	8	ADN47487	Adn47487	Thermococ	189	7	0.9	119	5	ABP07824	Abp07824	Human ORF
117	8	1.0	349	3	AAG49002	Aag49002	Arabidops	190	7	0.9	120	4	AAU40749	Aau40749	Proptonib
118	8	1.0	349	3	AAG49898	Aag49898	Arabidops	191	7	0.9	120	6	ABM37268	Abm37268	Proptonib
119	8	1.0	397	3	AAG49898	Aag49898	Arabidops	192	7	0.9	121	3	AAG14889	Aagi4889	Arabidops
120	8	1.0	409	3	AAG49001	Aag49001	Arabidops	193	7	0.9	122	4	AAM86629	Aam86629	Human imm
121	8	1.0	422	8	ADS23854	Ads23854	Bacterial	194	7	0.9	122	8	ADT57959	Adt57959	Plant pol
122	8	1.0	426	3	AAG48987	Aag48987	Arabidops	195	7	0.9	125	6	ABM69954	Abm69954	Phototrab
123	8	1.0	426	5	ABB93220	Abb93220	Herbicida	196	7	0.9	126	4	ABG69082	Abg69082	Drosophil
124	8	1.0	428	3	AAG14941	Aag14941	Arabidops	197	7	0.9	129	7	ADF04752	Adf04752	Bacterial
125	8	1.0	438	3	AAG14940	Aag14940	Arabidops	198	7	0.9	132	4	ABB11237	Abb11237	Human pho
126	8	1.0	445	4	ABG17863	Abg17863	Novel hum	199	7	0.9	143	3	AAG14888	Aagi4888	Arabidops
127	8	1.0	451	3	AAG06359	Aag06359	Arabidops	200	7	0.9	150	6	ABU26587	Abu26587	Protein e
128	8	1.0	454	3	AAG14939	Aag14939	Arabidops	201	7	0.9	157	7	ADF07373	Adf07373	Bacterial
129	8	1.0	461	3	AAG06358	Aag06358	Arabidops	202	7	0.9	170	3	AAG21405	Aag21405	Arabidops
130	8	1.0	479	3	AAG06357	Aag06357	Arabidops	203	7	0.9	171	6	ABU01664	Abu01664	S. pneumo
131	8	1.0	494	8	ADS24095	Ads24095	Bacterial	204	7	0.9	176	8	ADX79668	Adx79668	Plant ful
132	8	1.0	583	8	ADS14924	Ads14924	Pseudomon	205	7	0.9	176	9	AM97170	Am97170	M. xanthu
133	8	1.0	648	7	ABO75882	Abog75882	Pseudomon	206	7	0.9	178	2	AAV45288	Aay45288	Human sec
134	8	1.0	745	4	ABG03852	Abg03852	Novel hum	207	7	0.9	178	2	AAV30708	Aay30708	Amino aci
135	8	1.0	745	4	ABG09109	Abg09109	Novel hum	208	7	0.9	179	7	ABO75778	Abog75778	Pseudomon
136	8	1.0	745	4	ABG10367	Abg10367	Novel hum	209	7	0.9	181	9	ADM17088	Adm17088	Eucalyptu
137	8	1.0	745	4	ABG114360	Abg114360	Novel hum	210	7	0.9	182	3	AAG22490	Aag22490	Arabidops
138	8	1.0	897	8	ADP98989	Adp98989	C. albica	211	7	0.9	186	8	ADT58920	Adt58920	Plant pol
139	8	1.0	1577	6	ABU41145	Abu41145	Protein e	212	7	0.9	189	4	ABG23074	Abg23074	Novel hum
140	8	1.0	1589	7	ADF04713	Adf04713	Bacterial	213	7	0.9	190	8	ADU02422	Adu02422	Novel hum
141	7	0.9	7	4	AAU04432	Aau04432	Neisseria	214	7	0.9	193	7	ABO69082	Abog69082	Pseudomon
142	7	0.9	7	4	AAU04441	Aau04441	Neisseria	215	7	0.9	194	4	ADM20062	Adm20062	Protein e
143	7	0.9	7	4	AAU04446	Aau04446	Neisseria	216	7	0.9	195	5	ABU52193	Abu52193	Helicobac
144	7	0.9	7	4	AAU03969	Aau03969	Neisseria	217	7	0.9	195	8	ADP30464	Adp30464	Human sec
145	7	0.9	7	4	AAU04437	Aau04437	Neisseria	218	7	0.9	196	3	AAG22489	Aag22489	Arabidops
146	7	0.9	7	4	AAU04419	Aau04419	Neisseria	219	7	0.9	197	8	ADX73180	Adx73180	Plant ful
147	7	0.9	7	4	AAU04429	Aau04429	Neisseria	220	7	0.9	199	8	ADU17845	Adu17845	Reverse t
148	7	0.9	7	4	AAU04443	Aau04443	Neisseria	221	7	0.9	200	8	ADP30686	Adp30686	Human sec
149	7	0.9	7	4	AAU04433	Aau04433	Neisseria	222	7	0.9	208	4	ABG68565	Abg68565	Drosophil
150	7	0.9	23	3	AAV65830	Aay65830	Mismatch	223	7	0.9	213	7	ABO68534	Abog68534	Pseudomon
151	7	0.9	27	9	ADV53219	Adv53219	Hedgehog	224	7	0.9	213	8	ABO60429	Abog60429	Human gen
152	7	0.9	35	9	ADY97222	Ady97222	Herpes si	225	7	0.9	217	8	ADX68977	Adx68977	Plant ful
153	7	0.9	50	4	AAAM20158	Aam20158	Peptide #	226	7	0.9	219	9	ADZ64459	Adz64459	Human can
154	7	0.9	50	4	ABB40395	Abb40395	Peptide #	227	7	0.9	221	8	ADN25744	Adn25744	Bacterial
155	7	0.9	50	4	AAAM34101	Aam34101	Peptide #	228	7	0.9	226	4	ABG67771	Abg67771	Drosophil
156	7	0.9	50	4	ABB24767	Abb24767	Protein #	229	7	0.9	226	6	ABM68435	Abm68435	Phototrab
157	7	0.9	50	4	AAAM73922	Aam73922	Human bon	230	7	0.9	228	8	ADSA2499	Adsa2499	Bacterial
158	7	0.9	50	4	AAAM61203	Aam61203	Human bra	231	7	0.9	232	4	AAUS9216	Aaus9216	Proptonib
159	7	0.9	50	4	ABG55674	Abg55674	Human liv	232	7	0.9	232	6	ABM55735	Abm55735	Proptonib
160	7	0.9	50	5	ABG43810	Abg43810	Human pep	233	7	0.9	233	5	ABU51725	Abu51725	Helicobac
161	7	0.9	56	8	ADN46996	Adn46996	Thermococ	234	7	0.9	234	2	AAW98579	Aaw98579	H. pylori
162	7	0.9	58	2	AAW48931	Aaw48931	Schwannom	235	7	0.9	243	4	ABG24253	Abg24253	Novel hum
163	7	0.9	60	3	AAAG03150	Aag03150	Human sec	236	7	0.9	244	6	ABM70306	Abm70306	Phototrab
164	7	0.9	61	4	AAU65753	Aau65753	Proptonib	237	7	0.9	244	7	ABO67562	Abog67562	Klebsiell
165	7	0.9	61	6	ABM62272	Abm62272	Proptonib	238	7	0.9	250	4	ABBS9528	Abbs9528	Drosophil
166	7	0.9	69	4	AAAM88690	Aam88690	Human imm	239	7	0.9	253	8	ADL04906	Adl04906	M. catarr
167	7	0.9	75	7	ADC00302	Adc00302	Enterohae	240	7	0.9	255	8	ADM92238	Adm92238	S. pneumo
168	7	0.9	76	6	ABU15436	Abu15436	Protein e	241	7	0.9	255	8	ADM92238	Adm92238	S. pneumo
169	7	0.9	78	4	AAAM90288	Aam90288	Human imm	242	7	0.9	257	7	ABO82478	Abog82478	Pseudomon
170	7	0.9	82	5	ABP33075	Abp33075	Human ORF	243	7	0.9	260	9	ABM96630	Abm96630	M. xanthu

244	7	0.9	263	7	ABO77554	Pseudomon	317	7	0.9	357	7	ABO84393	Pseudomon
245	7	0.9	265	3	AAY95697	Cosmid cH	318	7	0.9	357	9	ABM93822	M. xanthu
246	7	0.9	268	7	ABO74392	Pseudomon	319	7	0.9	359	6	AAE36463	Human col
247	7	0.9	268	7	ABO83252	Pseudomon	320	7	0.9	359	8	ADP55871	Human PRO
248	7	0.9	268	7	ABO74393	Pseudomon	321	7	0.9	363	9	ADV67077	A. fumiga
249	7	0.9	270	7	ABO74440	Pseudomon	322	7	0.9	363	3	ABM96815	M. xanthu
250	7	0.9	277	8	ADQ81750	Trypanoso	323	7	0.9	366	2	ABM96392	Aspergill
251	7	0.9	277	8	AAY37752	Amino aci	324	7	0.9	366	8	ADN18365	Bacterial
252	7	0.9	280	5	ABP26998	Streptoco	325	7	0.9	367	7	ADM160171	Secreted
253	7	0.9	280	6	ABU46897	Protein e	326	7	0.9	379	7	ABM87030	Rice abio
254	7	0.9	282	6	ADA54528	Human pro	327	7	0.9	382	2	AAY45261	Human sec
255	7	0.9	282	7	ADC95911	E. faeciu	328	7	0.9	383	4	AAQ91116	C. Glutami
256	7	0.9	285	6	ABU45032	Protein e	329	7	0.9	386	4	ABG21113	Novel hum
257	7	0.9	288	2	AAR22996	Yeast pro	330	7	0.9	386	8	ADN26073	Bacterial
258	7	0.9	288	6	ARR53144	Protein s	331	7	0.9	387	7	ADI60400	Human sec
259	7	0.9	288	7	ADK63118	Disease t	332	7	0.9	387	9	ADP31368	Human sec
260	7	0.9	288	8	ADB44003	Bacterial	333	7	0.9	387	9	AEA21102	Novel hum
261	7	0.9	290	4	ABE110987	Human WD-	334	7	0.9	390	6	ABU20261	Protein e
262	7	0.9	290	4	AAM79660	Human pro	335	7	0.9	392	8	ADP29346	Human sec
263	7	0.9	291	7	ABO79608	Pseudomon	336	7	0.9	393	7	ABO68025	Pseudomon
264	7	0.9	292	6	ABU29077	Protein e	337	7	0.9	397	2	AAY29659	Homo sapi
265	7	0.9	293	8	ADS24291	Bacterial	338	7	0.9	398	8	ADY23747	Plant ful
266	7	0.9	294	7	ADC94620	E. faeciu	339	7	0.9	399	4	AAU32410	Novel hum
267	7	0.9	300	7	ABO63156	Klebsiell	340	7	0.9	399	7	ABO69686	Pseudomon
268	7	0.9	305	8	ADN17987	Bacterial	341	7	0.9	399	8	ADP31313	Human sec
269	7	0.9	310	3	AGS22488	Arabidops	342	7	0.9	405	4	AAAB93419	Human pro
270	7	0.9	310	8	ADS23653	Bacterial	343	7	0.9	405	8	ADN25996	Bacterial
271	7	0.9	310	9	ABM96413	M. xanthu	344	7	0.9	406	4	AAU39653	Human pol
272	7	0.9	310	9	AEA20290	Novel hum	345	7	0.9	409	6	AAU96684	Human nuc
273	7	0.9	314	3	AAQ221404	Arabidops	346	7	0.9	409	5	ABP29775	Streptoco
274	7	0.9	315	4	ABG74783	Human col	347	7	0.9	410	5	ABP30545	Streptoco
275	7	0.9	315	5	ABB91630	Herbicida	348	7	0.9	410	5	ABP30545	Streptoco
276	7	0.9	318	6	ABM67272	Photorhab	349	7	0.9	410	8	ADV89795	Streptoco
277	7	0.9	320	2	ABK33279	43 kD end	350	7	0.9	410	8	ADV83187	Streptoco
278	7	0.9	324	4	AAU38302	Salmonell	351	7	0.9	410	8	ADS23906	Bacterial
279	7	0.9	324	6	ABU48397	Protein e	352	7	0.9	411	8	ADS23906	Bacterial
280	7	0.9	325	4	AAU79630	Corynebac	353	7	0.9	413	4	AAU41340	Propionib
281	7	0.9	325	4	AAU91087	C. glutami	354	7	0.9	413	6	ABM94363	Propionib
282	7	0.9	327	5	ABM89542	Human pol	355	7	0.9	416	6	ABU42300	Protein e
283	7	0.9	327	7	ABO81872	Pseudomon	356	7	0.9	416	6	ABM72077	Staphyloc
284	7	0.9	328	5	ABU51082	Helicobac	357	7	0.9	417	4	ABG03334	Novel hum
285	7	0.9	329	3	ABM52512	Helicobac	358	7	0.9	417	5	ABP27080	Streptoco
286	7	0.9	335	5	AAU93075	Arabidops	359	7	0.9	418	5	ABP27080	Streptoco
287	7	0.9	335	7	ADD30801	Plant yie	360	7	0.9	420	4	ABM62035	P. furios
288	7	0.9	335	8	ADI41831	Murine tra	361	7	0.9	420	4	ABM62035	P. furios
289	7	0.9	336	8	ADI27927	Streptoco	362	7	0.9	423	4	ABG28086	Novel hum
290	7	0.9	337	3	AAI96738	Streptoco	363	7	0.9	423	4	ABG28086	Novel hum
291	7	0.9	337	5	ABP26971	Streptoco	364	7	0.9	425	3	AAU44389	Zea may
292	7	0.9	337	5	ABP26970	Streptoco	365	7	0.9	425	3	AAU44389	Zea may
293	7	0.9	337	5	ABB90355	Human pol	366	7	0.9	426	8	ADN21982	Bacterial
294	7	0.9	337	6	ABU46738	Protein e	367	7	0.9	426	8	ADN21982	Bacterial
295	7	0.9	337	8	ADV87896	Streptoco	368	7	0.9	429	6	ABU232542	Protein e
296	7	0.9	337	8	ADV81346	Streptoco	369	7	0.9	430	6	ABM686599	Photorhab
297	7	0.9	337	8	ADV79149	Streptoco	370	7	0.9	432	4	AAU96771	Putative
298	7	0.9	337	9	ADY19066	PRO polyp	371	7	0.9	432	4	AAU96771	Putative
299	7	0.9	337	9	ADY20473	PRO polyp	372	7	0.9	434	7	ABO78489	Protein e
300	7	0.9	341	4	ABG65050	Drosophil	373	7	0.9	434	7	ABO78489	Protein e
301	7	0.9	341	4	ABG17128	Novel hum	374	7	0.9	434	7	ABO78489	Protein e
302	7	0.9	342	5	ADN19670	Human dru	375	7	0.9	444	4	ABU03821	Helicobac
303	7	0.9	349	6	ABU23963	Protein e	376	7	0.9	444	4	ABU03821	Helicobac
304	7	0.9	351	7	ABO62898	Klebsiell	377	7	0.9	444	8	ADN24258	Bacterial
305	7	0.9	351	8	ADN21155	Bacterial	378	7	0.9	444	8	ADN24258	Bacterial
306	7	0.9	351	8	ADN21155	Bacterial	379	7	0.9	448	8	ADN21452	Bacterial
307	7	0.9	352	8	ABM83397	Human dia	380	7	0.9	448	8	ADN21452	Bacterial
308	7	0.9	352	9	ADV50410	Human dia	381	7	0.9	456	8	ADP31476	Human sec
309	7	0.9	353	8	ABM83396	Human dia	382	7	0.9	456	8	ADP31476	Human sec
310	7	0.9	353	8	ABM83396	Human dia	383	7	0.9	458	5	ABE23295	Human nec
311	7	0.9	355	2	AAR74758	Beta-keto	384	7	0.9	459	6	ABU22029	Protein e
312	7	0.9	355	6	ABM73087	Staphyloc	385	7	0.9	459	6	ABU22029	Protein e
313	7	0.9	355	6	ABM73087	Staphyloc	386	7	0.9	459	6	ABU22029	Protein e
314	7	0.9	355	6	AAE38417	Arabidops	387	7	0.9	460	4	AAU41439	Human pol
315	7	0.9	355	6	ABU24320	Protein e	388	7	0.9	464	3	AAU15924	E. coli p
316	7	0.9	356	6	ABU24320	Protein e	389	7	0.9	464	4	AAU15924	E. coli g

390	7	0.9	464	6	ABU14689	Abu14689 Protein e	463	7	0.9	590	8	ADU25434	Adu25434 L. acidop
391	7	0.9	464	7	ADC31497	Adc31497 Human nov	464	7	0.9	596	8	ADN99873	Adn99873 Novel hum
392	7	0.9	465	7	ABO80641	AbO80641 Pseudomon	465	7	0.9	596	8	ADN99872	Adn99872 Novel hum
393	7	0.9	465	9	ADY86239	Ady86239 B. napus	466	7	0.9	609	3	AY73487	Aay73487 Human sec
394	7	0.9	466	4	AAU62912	Aau62912 Propionib	467	7	0.9	614	6	ADA33217	Adh33217 Acinetoba
395	7	0.9	466	6	ABM59431	Abm59431 Propionib	468	7	0.9	614	8	ADH48376	Adh48376 Human KPP
396	7	0.9	469	8	ADS24348	AdS24348 Bacterial	469	7	0.9	619	8	ADN23202	Adn23202 Bacterial
397	7	0.9	472	3	AAB18420	Aab18420 Amino aci	470	7	0.9	620	2	AAR77275	Aar77275 ORC2 subu
398	7	0.9	473	6	ADA33992	Ada33992 Acinetoba	471	7	0.9	620	2	AAW22225	Aaw22225 S. cerevi
399	7	0.9	478	4	ABB66297	Abb66297 Drosophil	472	7	0.9	620	5	AAU82999	Aau82999 S. cerevi
400	7	0.9	478	5	ABR38839	AbR38839 A. niger	473	7	0.9	620	6	ABR53643	Abr53643 Protein s
401	7	0.9	482	4	ADM19812	Adm19812 Protein e	474	7	0.9	620	7	ADK64130	Adk64130 Disease t
402	7	0.9	485	5	ADJ33852	Adj33852 Protein o	475	7	0.9	621	7	ADN18789	Adn18789 Bacterial
403	7	0.9	490	2	AY33929	Aay33929 Leukotoxi	476	7	0.9	621	7	ABO70379	AbO70379 Pseudomon
404	7	0.9	490	6	ADA28694	Ada28694 Plasmid p	477	7	0.9	622	5	ABF61455	Abf61455 Human NF-
405	7	0.9	494	9	AEB27284	Aeb27284 Pinus rad	478	7	0.9	622	6	ABR41036	Abr41036 Human MAP
406	7	0.9	497	4	AAU37751	Aau37751 Streptoco	479	7	0.9	623	4	AAW79912	Aam79912 Human pro
407	7	0.9	497	6	ABU01284	Abu01284 S. pneumo	480	7	0.9	623	4	AAW79913	Aam79913 Human pro
408	7	0.9	497	6	ABU45988	Abu45988 Protein e	481	7	0.9	625	8	ADK44452	Adk44452 Bacterial
409	7	0.9	497	8	ADK48573	Adk48573 Streptoco	482	7	0.9	627	4	ABG18262	Abg18262 Novel hum
410	7	0.9	497	8	ADM92139	Adm92139 S. pneumon	483	7	0.9	628	4	ABG23677	Abg23677 Novel hum
411	7	0.9	504	8	ADR95097	Adr95097 Novel S.	484	7	0.9	632	5	AAO19378	Aao19378 Human NF-
412	7	0.9	504	9	AEA58967	Aea58967 Streptoco	485	7	0.9	632	5	ABP61456	Abp61456 Human pal
413	7	0.9	514	6	ABJ20237	Abj20237 Human IG	486	7	0.9	649	4	ABE61237	AbE61237 Drosophil
414	7	0.9	517	3	AAJ32390	Aaj32390 Herpesvir	487	7	0.9	662	9	AEA24005	Aea24005 Human PRO
415	7	0.9	517	5	AAE23294	Aae23294 Human nec	488	7	0.9	663	6	ABU24491	Abu24491 Protein e
416	7	0.9	518	5	ABG77170	Abg77170 Prostate	489	7	0.9	665	4	AAW78876	Aaw78876 Human pro
417	7	0.9	518	8	ADS29669	AdS29669 Bacterial	490	7	0.9	665	9	ADY17134	Ady17134 PRO polyp
418	7	0.9	518	6	ABU85769	Abu85769 Human pro	491	7	0.9	666	4	AAW79657	Aaw79657 Corynebac
419	7	0.9	521	6	ABU35710	Abu35710 Protein e	492	7	0.9	666	4	AAU71885	Aau71885 C. glutam
420	7	0.9	522	6	ABU22090	Abu22090 Protein e	493	7	0.9	667	4	ABG16901	Abg16901 Novel hum
421	7	0.9	527	6	ABU19551	Abu19551 Protein e	494	7	0.9	667	4	AAU32908	Aau32908 Novel hum
422	7	0.9	528	4	ABW71669	Abw71669 Drosophil	495	7	0.9	671	2	AAW38505	Aaw38505 Streptoco
423	7	0.9	529	8	ADC61129	Adc61129 Baeyer-Vi	496	7	0.9	671	2	AAW85917	Aay85917 S. pneumo
424	7	0.9	529	8	ADT59473	Adt59473 Plant pol	497	7	0.9	671	8	ADK47127	Adk47127 Streptoco
425	7	0.9	531	8	ADP30594	Adp30594 Human sec	498	7	0.9	673	5	AAE25082	Aae25082 Human kin
426	7	0.9	531	8	ADP31696	Adp31696 Human sec	499	7	0.9	676	8	ADR95463	Adr95463 Novel S.
427	7	0.9	544	2	AAW03943	Aaw03943 LKT-GnRH	500	7	0.9	676	9	AEA59333	Aea59333 Streptoco
428	7	0.9	544	2	AAW79570	Aaw79570 LKT-GnRH	501	7	0.9	686	6	ABU39853	Abu39853 Protein e
429	7	0.9	549	9	ADM70886	Adm70886 Aspergill	502	7	0.9	692	8	ADN26147	Adn26147 Bacterial
430	7	0.9	549	9	ADZ64458	Adz64458 Human can	503	7	0.9	695	2	AAW79573	Aaw79573 LKT-GnRH
431	7	0.9	551	8	ADO65217	Ado65217 Novel hum	504	7	0.9	695	3	AAV58361	Aay58361 Leukotoxi
432	7	0.9	559	7	ABO75946	AbO75946 Pseudomon	505	7	0.9	695	3	AAV58133	Aay58133 Gonadotro
433	7	0.9	560	4	AAW78929	Aam78929 Human pro	506	7	0.9	699	7	ABO68327	AbO68327 Pseudomon
434	7	0.9	562	4	ABB64878	Abb64878 Drosophil	507	7	0.9	702	5	ABP56679	Abp56679 Bifidobac
435	7	0.9	564	6	ABJ37094	Abj37094 Low-affin	508	7	0.9	705	4	AAW79860	Aam79860 Human pro
436	7	0.9	564	8	ADT59636	Adt59636 Plant pol	509	7	0.9	705	8	ADP30746	Adp30746 Human sec
437	7	0.9	566	6	AAE35922	Aae35922 Human All	510	7	0.9	710	8	ADX77146	Adx77146 Plant ful
438	7	0.9	568	5	ABU51967	Abu51967 Helicobac	511	7	0.9	711	8	ADP32237	Adp32237 Plant ful
439	7	0.9	568	5	ABP74083	Abp74083 Candida a	512	7	0.9	717	4	ABB61609	Abb61609 Drosophil
440	7	0.9	572	6	ABJ37095	Abj37095 Low-affin	513	7	0.9	717	8	ADO07924	Ado07924 Fly polyp
441	7	0.9	572	7	ADC07800	Adc07800 Rice prot	514	7	0.9	731	5	ABU52070	Abu52070 Helicobac
442	7	0.9	572	7	ADF74126	Adf74126 Human nov	515	7	0.9	741	6	ABU42146	Abu42146 Protein e
443	7	0.9	573	4	ABB60673	Abb60673 Drosophil	516	7	0.9	742	9	ADZ64457	Adz64457 Human can
444	7	0.9	576	7	ABO74500	AbO74500 Pseudomon	517	7	0.9	745	9	AEA26999	Aea26999 Stress to
445	7	0.9	578	8	ADP03592	Adp03592 Infection	518	7	0.9	759	7	ABM98120	Abm98120 Rice abio
446	7	0.9	579	4	ABG24250	Abg24250 Novel hum	519	7	0.9	761	5	ABB77431	Abb77431 Human tum
447	7	0.9	580	5	AAAG6008	Aag66008 F. necrop	520	7	0.9	792	4	ABG15703	Abg15703 Novel hum
448	7	0.9	580	8	ADO47877	Ado47877 Alpha-Her	521	7	0.9	792	7	ABM85854	Abm85854 Mouse pro
449	7	0.9	581	8	ADP03590	Adp03590 Infection	522	7	0.9	792	8	ADH12911	Adh12911 Francisel
450	7	0.9	584	6	ABU19765	Abu19765 Protein e	523	7	0.9	797	8	ADS23447	AdS23447 Bacterial
451	7	0.9	587	4	AAW78928	Aam78928 Human pro	524	7	0.9	799	3	AAV92061	Aay92061 Human APC
452	7	0.9	587	5	AAU82982	Aau82982 Human hom	525	7	0.9	809	2	AAV29672	Aay29672 Human cer
453	7	0.9	587	5	AAU10799	Aau10799 Polymorph	526	7	0.9	816	8	ADP31581	Adp31581 Human sec
454	7	0.9	587	5	AAU10796	Aau10796 Reference	527	7	0.9	818	4	AAO92737	Aag92737 C glutami
455	7	0.9	587	5	AAU10797	Aau10797 Polymorph	528	7	0.9	821	7	ABO72267	AbO72267 Pseudomon
456	7	0.9	587	5	AAU10798	Aau10798 Polymorph	529	7	0.9	823	4	ABB71484	Abb71484 Drosophil
457	7	0.9	587	8	ADL17020	Adl17020 Human Ran	530	7	0.9	827	7	ADF06140	Adf06140 Bacterial
458	7	0.9	587	8	ADO88017	Ado88017 Human Ran	531	7	0.9	850	4	ABBS2809	Abbs2809 Escherich
459	7	0.9	587	8	ABM82366	Abm82366 Tumour-as	532	7	0.9	861	8	ADP31340	Adp31340 Human sec
460	7	0.9	587	9	ADY19712	Ady19712 PRO polyp	533	7	0.9	870	8	ADP30646	Adp30646 Human sec
461	7	0.9	587	9	ADY16715	Ady16715 PRO polyp	534	7	0.9	874	6	ABU33564	Abu33564 Protein e
462	7	0.9	589	7	ADB85263	Abd85263 Mouse RNA	535	7	0.9	892	8	ADP31578	Adp31578 Human sec

536	7	0.9	897	4	ABB62261	Abb62261 Drosophil	609	7	0.9	1132	7	ADD71144	Add71144 Human int
537	7	0.9	908	6	ABU08492	Abu08492 Alpha-hel	610	7	0.9	1136	6	ABU08605	Abu08605 Neisseria
538	7	0.9	914	6	ABU08604	Abu08604 Neisseria	611	7	0.9	1139	5	ABG97360	Abg97360 Human CGD
539	7	0.9	921	2	AAW72033	Aaw72033 HSV-2 str	612	7	0.9	1156	3	AB101014	Ab101014 Feline fcd
540	7	0.9	921	9	ABE37187	Aeb37187 L. pneumo	613	7	0.9	1161	5	ABG97354	Abg97354 Human CGD
541	7	0.9	921	9	ABE40526	Aeb40526 L. pneumo	614	7	0.9	1168	5	ADZ64434	Adz64434 Human can
542	7	0.9	924	2	AAW10889	Aar10889 Leukotoxi	615	7	0.9	1178	6	ABU08603	Abu08603 Neisseria
543	7	0.9	924	2	AAW42378	Aar42378 Recombina	616	7	0.9	1187	8	ADJ49198	Adj49198 Oll-assoc
544	7	0.9	924	2	AAW42380	Aar42380 Recombina	617	7	0.9	1197	8	ADP31342	Adp31342 Human sec
545	7	0.9	924	2	AAW42385	Aar42385 Recombina	618	7	0.9	1216	5	AAE22860	Aae22860 Human pho
546	7	0.9	925	5	AAO14246	Aao14246 Human pre	619	7	0.9	1268	4	ABB61314	Abb61314 Drosophil
547	7	0.9	926	2	AAW14482	Aar14482 LKT352.1	620	7	0.9	1296	2	ADP31500	Adp31500 Human sec
548	7	0.9	926	2	AAW14482	Aar14482 LKT352.1	621	7	0.9	1320	5	AAW47603	Aaw47603 Drosophil
549	7	0.9	926	2	AAW34545	Aar34545 Leukotoxi	622	7	0.9	1334	2	AAW47157	Aaw47157 Nevoid ba
550	7	0.9	926	2	AAW50291	Aar50291 Recombina	623	7	0.9	1334	2	AAW47157	Aaw47157 Nevoid ba
551	7	0.9	926	2	AAW03945	Aaw03945 P. haemol	624	7	0.9	1334	2	AAW47157	Aaw47157 Nevoid ba
552	7	0.9	926	2	AAW03945	Aaw03945 P. haemol	625	7	0.9	1336	7	ADJ92014	Adj92014 Human can
553	7	0.9	932	8	ADR08677	Adr08677 Human pro	626	7	0.9	1372	9	ADZ64453	Adz64453 Human can
554	7	0.9	933	7	ABM85855	Abm85855 Human pro	627	7	0.9	1380	9	ADZ64452	Adz64452 Human can
555	7	0.9	933	8	ADN03759	Adn03759 Antipsori	628	7	0.9	1390	6	ABP60436	Abp60436 Human and
556	7	0.9	933	8	ADN03759	Adn03759 Antipsori	629	7	0.9	1390	9	ADW02021	Adw02021 Human MPT
557	7	0.9	934	2	AAW07637	Aaw07637 P. suis 1	630	7	0.9	1390	9	ADY17478	Ady17478 PRO polyv
558	7	0.9	936	2	AAW34547	Aar34547 GnRH-leuk	631	7	0.9	1390	9	ADY17963	Ady17963 PRO polyv
559	7	0.9	937	8	ADH13664	Adh13664 Human ENZ	632	7	0.9	1390	9	ADZ64450	Adz64450 Human can
560	7	0.9	939	9	ADZ64455	Adz64455 Human can	633	7	0.9	1396	8	ADN01130	Adn01130 Human cel
561	7	0.9	943	2	AAW34546	Aar34546 Somatosta	634	7	0.9	1403	2	AAW10890	Aar10890 lktA::lac
562	7	0.9	949	4	ABW68553	Abw68553 Human GTP	635	7	0.9	1403	2	AAW79574	Aaw79574 Leukotoxi
563	7	0.9	950	4	AAW73355	Aaw73355 Human mes	636	7	0.9	1419	5	ABU65081	Abu65081 Human NOV
564	7	0.9	951	2	AAW34548	Aar34548 Rotavirus	637	7	0.9	1419	5	ADH42427	Adh42427 Novel hum
565	7	0.9	951	2	AAW34548	Aar34548 Rotavirus	638	7	0.9	1419	5	ADH42427	Adh42427 Novel hum
566	7	0.9	951	4	AAW73356	Aaw73356 Rat meg-1	639	7	0.9	1423	8	ADH42431	Adh42431 Novel hum
567	7	0.9	953	2	AAW07167	Aar07167 105KD PTX	640	7	0.9	1423	8	ADN61817	Adn61817 Human lip
568	7	0.9	953	2	AAW15159	Aar15159 Leukotoxi	641	7	0.9	1433	8	ADO18815	Ado18815 Human lip
569	7	0.9	953	2	AAW43865	Aaw43865 Leukotoxi	642	7	0.9	1433	8	ADO18815	Ado18815 Human lip
570	7	0.9	953	2	AAW60072	Aaw60072 FtxA prot	643	7	0.9	1434	2	AAW94380	Aaw94380 Mouse pat
571	7	0.9	953	2	AAW60072	Aaw60072 FtxA prot	644	7	0.9	1434	2	AAW52199	Aaw52199 Mouse pat
572	7	0.9	956	6	ABU08602	Abu08602 Neisseria	645	7	0.9	1434	2	AAW72968	Aaw72968 Mouse pat
573	7	0.9	963	7	ADB67089	Adb67089 Kinesin h	646	7	0.9	1434	4	AAW67159	Aaw67159 Murine pa
574	7	0.9	963	7	ADB67091	Adb67091 Kinesin h	647	7	0.9	1434	5	AAW79572	Aaw79572 Mouse pat
575	7	0.9	963	9	ABE08391	Abe08391 c-Jun inh	648	7	0.9	1434	7	ABU62271	Abu62271 Murine pt
576	7	0.9	964	8	ADL99362	Adl99362 Nanostroc	649	7	0.9	1434	7	ADH62722	Adh62722 Mouse pat
577	7	0.9	964	8	ADL99362	Adl99362 Nanostroc	650	7	0.9	1434	8	ADE48980	Ade48980 Mouse pat
578	7	0.9	967	6	AAW80245	Aaw80245 Human lip	651	7	0.9	1439	4	AAU27557	Aau27557 Neisseria
579	7	0.9	969	6	AAW34448	Aaw34448 Human lip	652	7	0.9	1447	2	AAW75375	Aaw75375 Human pat
580	7	0.9	977	2	AAW03942	Aaw03942 LKT-GnRH	653	7	0.9	1447	2	AAW52200	Aaw52200 Human pat
581	7	0.9	977	2	AAW03942	Aaw03942 LKT-GnRH	654	7	0.9	1447	2	AAW72969	Aaw72969 Human pat
582	7	0.9	978	7	ADM05468	Adm05468 Human pro	655	7	0.9	1447	2	AAW67163	Aaw67163 Human pat
583	7	0.9	979	9	ABE49457	Aeb49457 N. mening	656	7	0.9	1447	5	AAE19830	Aae19830 Human pat
584	7	0.9	979	9	ABE49457	Aeb49457 N. mening	657	7	0.9	1447	5	ABJ10931	Abj10931 TRC8 rela
585	7	0.9	983	5	ABW77509	Abw77509 Tranetes	658	7	0.9	1447	5	AAW79571	Aaw79571 Human pat
586	7	0.9	998	2	AAW38822	Aay38822 Neisseria	659	7	0.9	1447	5	ABU62275	Abu62275 Human pat
587	7	0.9	1004	8	ADO18816	Ado18816 Human lip	660	7	0.9	1447	7	ADU66678	Adu66678 Human pro
588	7	0.9	1016	6	ABU41567	Abu41567 Protein e	661	7	0.9	1447	7	ADH62731	Adh62731 Human pat
589	7	0.9	1016	6	ABU41567	Abu41567 Protein e	662	7	0.9	1447	7	ADH62731	Adh62731 Human pat
590	7	0.9	1017	8	ADP31268	Adp31268 Human sec	663	7	0.9	1447	8	ADE48989	Ade48989 Human pat
591	7	0.9	1019	8	ADJ69855	Adj69855 Human hea	664	7	0.9	1449	2	AAW38824	Aaw38824 Neisseria
592	7	0.9	1050	8	ADP31376	Adp31376 Human sec	665	7	0.9	1449	2	AAW38824	Aaw38824 Neisseria
593	7	0.9	1054	5	AAW79311	Aaw79311 Human ova	666	7	0.9	1449	6	ABU37787	Abu37787 Protein e
594	7	0.9	1069	2	AAW52748	Aaw52748 Bovine IF	667	7	0.9	1449	9	ABE49461	Aeb49461 N. mening
595	7	0.9	1069	2	AAW13867	Aaw13867 Chimeric	668	7	0.9	1454	3	AAW56621	Aaw56621 Neisseria
596	7	0.9	1069	3	AAW21074	Aaw21074 Bovine ga	669	7	0.9	1454	3	AAW56621	Aaw56621 Neisseria
597	7	0.9	1076	5	ABP69070	Abp69070 Human pol	670	7	0.9	1457	3	AAW56622	Aaw56622 Neisseria
598	7	0.9	1078	4	ABW61597	Abw61597 Drosophil	671	7	0.9	1457	3	AAW56622	Aaw56622 Neisseria
599	7	0.9	1088	4	ABW78676	Abw78676 Human pro	672	7	0.9	1457	3	AAW56622	Aaw56622 Neisseria
600	7	0.9	1098	2	AAW22103	Aar22103 Bovine IL	673	7	0.9	1457	3	AAW56622	Aaw56622 Neisseria
601	7	0.9	1098	2	AAW22103	Aar22103 Bovine IL	674	7	0.9	1457	3	AAW56622	Aaw56622 Neisseria
602	7	0.9	1098	2	AAW13866	Aaw13866 Chimeric	675	7	0.9	1457	6	ABU08601	Abu08601 Neisseria
603	7	0.9	1098	3	AAW21073	Aaw21073 Bovine IL	676	7	0.9	1457	6	ABU08601	Abu08601 Neisseria
604	7	0.9	1116	8	ADP31692	Adp31692 Human sec	677	7	0.9	1458	5	ABW09556	Abw09556 Human lip
605	7	0.9	1121	8	AAE20419	Aae20419 Human cdc	678	7	0.9	1458	5	ABW09556	Abw09556 Human lip
606	7	0.9	1121	8	ADJ66576	Adj66576 WD-repeat	679	7	0.9	1458	6	ABW34440	Abw34440 Human lip
607	7	0.9	1129	7	ABO79806	Abw79806 Pseudomon	680	7	0.9	1464	8	ADP31437	Adp31437 Human sec
608	7	0.9	1132	2	AAW77417	Aaw77417 Human cel	681	7	0.9	1468	2	AAW38825	Aay38825 Neisseria

682	7	0.9	1468	6	ABP77279	Abp77279	N. gonorr	755	6	0.8	9	5	ABB95084	CTL epit
683	7	0.9	1468	6	ABU37103	Abu37103	Protein e	756	6	0.8	9	5	ABB94690	CTL epit
684	7	0.9	1468	9	ADV99673	Adv99673	Neisseria	757	6	0.8	9	5	ADP21237	Absorptio
685	7	0.9	1468	9	AEb49463	Aeb49463	N. gonorr	758	6	0.8	9	8	ADP25609	Plasmodiu
686	7	0.9	1628	4	ABG02195	Abg02195	Novel hum	759	6	0.8	9	9	ADZ50442	Y. pestis
687	7	0.9	1633	9	ABM93693	Abm93693	M. xanthu	760	6	0.8	9	9	ADZ81870	Human lam
688	7	0.9	1686	2	AAW70991	Aaw70991	Human cla	761	6	0.8	10	2	AAZ33824	Selectin
689	7	0.9	1686	6	ABJ19811	Abj19811	Androgen-	762	6	0.8	10	2	AAZ33825	Selectin
690	7	0.9	1725	8	ADP30654	Adp30654	Human sec	763	6	0.8	10	2	AAZ33833	Selectin
691	7	0.9	1833	8	ADP30642	Adp30642	Human sec	764	6	0.8	10	2	AAZ33834	Selectin
692	7	0.9	1846	6	ABR33983	Abr33983	Human SCA	765	6	0.8	10	2	AAZ50817	Cyclic pe
693	7	0.9	1895	2	AAW72095	Aaw72095	HSV-2 str	766	6	0.8	10	4	AAZ94318	Human com
694	7	0.9	1912	7	ADC26223	Adc26223	Human NOV	767	6	0.8	10	4	AAZ94318	Human com
695	7	0.9	1943	6	ABU30826	Abu30826	Protein e	768	6	0.8	10	4	AAZ95396	Saccharom
696	7	0.9	1956	8	ADN00371	Adn00371	Novel hum	769	6	0.8	10	5	AAZ95044	CTL epit
697	7	0.9	1956	8	ABE13352	Aeb13352	KTAAL1000	770	6	0.8	10	5	ABZ94737	CTL epit
698	7	0.9	1974	2	AAW98391	Aaw98391	H. pylori	771	6	0.8	10	5	ABZ94739	CTL epit
699	7	0.9	1984	4	ABG01338	Abg01338	Novel hum	772	6	0.8	10	5	ABZ94944	CTL epit
700	7	0.9	2223	8	ADV99896	Adv99896	Nanchangm	773	6	0.8	10	5	ABZ94629	CTL epit
701	7	0.9	2274	4	AAZ50674	Aaz50674	Mouse APC	774	6	0.8	10	5	ADK06129	Hepatitib
702	7	0.9	2274	8	ADO08047	Ado08047	Mouse pol	775	6	0.8	11	9	ADV14170	Yeast N-t
703	7	0.9	2274	8	ADZ85091	Adz85091	Full1-leng	776	6	0.8	12	2	AAZ21275	Human sem
704	7	0.9	2303	6	ABZ58648	Abr58648	Human can	777	6	0.8	12	6	ABZ98955	ErbB2 cel
705	7	0.9	2303	8	ADO08045	Ado08045	Human pol	778	6	0.8	12	9	ADZ81833	Human lam
706	7	0.9	2303	8	ADV70185	Adv70185	Tumor-ass	779	6	0.8	12	9	AEA18385	Peptide u
707	7	0.9	2338	8	ABO58348	Abo58348	Human gen	780	6	0.8	13	2	AAW23015	R4 recept
708	7	0.9	2349	8	ADP30959	Adp30959	Human sec	781	6	0.8	13	6	ABZ98589	Beta-barr
709	7	0.9	2382	8	ADP31341	Adp31341	Human sec	782	6	0.8	14	4	ABZ56739	Human SNP
710	7	0.9	2431	2	AAZ25138	Aaz25138	SPV4 non-	783	6	0.8	15	5	ABP46959	Human Bly
711	7	0.9	2732	4	ABZ52855	Abz52855	Escherich	784	6	0.8	15	7	ADZ32583	Clostridi
712	7	0.9	2834	5	ABG97576	Abg97576	Haemagglu	785	6	0.8	15	7	ADG97786	scFV VHCD
713	7	0.9	2834	4	ADH80652	Adh80652	Escherich	786	6	0.8	15	9	ADW10966	Human pho
714	7	0.9	3119	2	AAW72204	Aaw72204	HSV-2 str	787	6	0.8	16	9	ADV13047	Human pho
715	7	0.9	3122	7	ADG75178	Adg75178	Human her	788	6	0.8	18	2	AAW40133	Delta'S s
716	7	0.9	3122	7	ADG75129	Adg75129	Human her	789	6	0.8	18	2	AAW36080	E. coli D
717	7	0.9	3194	6	ABU31122	Abu31122	Protein e	790	6	0.8	18	8	ADL15120	E. coli D
718	7	0.9	3194	9	ABZ91380	Abz91380	Microbial	791	6	0.8	18	9	ADZ11758	E. coli D
719	7	0.9	3339	8	ADP31219	Adp31219	Human sec	792	6	0.8	19	2	AAW46341	Amino aci
720	7	0.9	3407	8	ADP31060	Adp31060	Human sec	793	6	0.8	19	5	ABO74114	Plasmid p
721	7	0.9	3407	8	ADP31062	Adp31062	Human sec	794	6	0.8	19	5	AAO19110	Human cir
722	7	0.9	3455	8	ADV99914	Adv99914	Nanchangm	795	6	0.8	20	2	AAW22332	HIV-1 cli
723	7	0.9	3477	8	ADP30704	Adp30704	Human sec	796	6	0.8	20	2	AAW62895	Peptide s
724	7	0.9	3579	8	ADP31098	Adp31098	Human sec	797	6	0.8	21	3	AAZ56865	B. catarr
725	7	0.9	3956	8	ADV99898	Adv99898	Nanchangm	798	6	0.8	21	3	AAZ56865	B. catarr
726	7	0.9	4106	4	ABG99872	Abg99872	S. cinnam	799	6	0.8	21	7	ADC73122	Domain l1
727	7	0.9	4752	8	ADP30585	Adp30585	Human sec	800	6	0.8	22	4	AAZ83929	Antigenic
728	7	0.9	4752	8	ADP30651	Adp30651	Human sec	801	6	0.8	22	6	ADA11828	Human nov
729	7	0.9	4999	5	AAO22158	Aao22158	Ramoplani	802	6	0.8	23	9	ADZ86384	Protein q
730	7	0.9	5304	8	ADP30706	Adp30706	Human sec	803	6	0.8	23	9	AEZ25314	Synthetic
731	7	0.9	6465	8	ADP30705	Adp30705	Human sec	804	6	0.8	23	9	AEZ25313	Synthetic
732	7	0.9	8026	6	AAE35489	Aae35489	Streptomy	805	6	0.8	24	5	AAU73141	Parathyro
733	7	0.9	8976	8	ADP31425	Adp31425	Human sec	806	6	0.8	24	5	AAU73142	Parathyro
734	7	0.9	9195	8	ADP31494	Adp31494	Human sec	807	6	0.8	24	8	ADQ75456	PTH/PTHrP
735	7	0.9	10944	8	ADP31311	Adp31311	Human sec	808	6	0.8	24	8	ADQ75457	PTH/PTHrP
736	7	0.9	11328	8	ADP31310	Adp31310	Human sec	809	6	0.8	25	9	ADV16640	E. faecal
737	7	0.9	36946	9	ADV97835	Adv97835	Murine pr	810	6	0.8	26	4	AAW99735	Human exc
738	6	0.8	6	4	AAU03972	Aau03972	Neisseria	811	6	0.8	26	4	AAW42550	Human kid
739	6	0.8	6	4	AAU03989	Aau03989	Neisseria	812	6	0.8	26	9	AEZ25322	Synthetic
740	6	0.8	6	4	AAU04415	Aau04415	Neisseria	813	6	0.8	28	2	AAW54400	MAGE-10 t
741	6	0.8	6	4	AAU03962	Aau03962	Neisseria	814	6	0.8	28	3	AAZ65042	Human 5'
742	6	0.8	6	4	AAU03968	Aau03968	Neisseria	815	6	0.8	28	3	AAZ65042	Human 5'
743	6	0.8	6	4	AAU04431	Aau04431	Neisseria	816	6	0.8	28	3	AAZ65042	Human 5'
744	6	0.8	6	4	AAU03983	Aau03983	Neisseria	817	6	0.8	28	5	AAU73105	Parathyro
745	6	0.8	7	2	AAZ44781	Aaz44781	Sequence	818	6	0.8	28	5	AAU73106	Parathyro
746	6	0.8	7	2	AAZ44782	Aaz44782	Sequence	819	6	0.8	28	8	ADQ75421	PTH/PTHrP
747	6	0.8	7	4	AAZ62826	Aaz62826	Fibrinoge	820	6	0.8	28	8	ADQ75420	PTH/PTHrP
748	6	0.8	7	4	AAZ62823	Aaz62823	Fibrinoge	821	6	0.8	28	8	ADU72606	Signal pe
749	6	0.8	7	5	AAO21220	Aao21220	Absorptio	822	6	0.8	28	9	ADZ73597	Human inc
750	6	0.8	8	2	AAZ73428	Aaz73428	Human TSH	823	6	0.8	29	6	ABJ26817	Endotheli
751	6	0.8	8	5	AAO21222	Aao21222	Absorptio	824	6	0.8	29	6	ABZ29400	Streptoco
752	6	0.8	9	2	AAZ25260	Aaz25260	HIV Env g	825	6	0.8	30	5	AAU73170	Parathyro
753	6	0.8	9	5	ABZ94918	Abz94918	CTL epit	826	6	0.8	30	5	AAU73136	Parathyro
754	6	0.8	9	5	ABZ94587	Abz94587	CTL epit	827	6	0.8	30	5	AAU73137	Parathyro

828	6	0.8	30	8	ADQ75451	Adq75451 PTH/PTHrP	901	6	0.8	40	5	AAE25415	Aae25415 ZYMW AGII
829	6	0.8	30	8	ADQ75485	Adq75485 PTH/PTHrP	902	6	0.8	40	8	ADS05943	Ads05943 Staphyloc
830	6	0.8	30	8	ADQ75452	Adq75452 PTH/PTHrP	903	6	0.8	41	2	AY85919	AY85919 S. pneumo
831	6	0.8	31	2	AA04222	Aay04222 Human par	904	6	0.8	41	2	AY01637	Aay01637 Human PS2
832	6	0.8	31	5	ABB57410	Abd57410 Human sec	905	6	0.8	42	4	AAU14818	Aau14818 Novel bon
833	6	0.8	31	7	AD124798	Adi24798 Parathyro	906	6	0.8	43	4	AAE04543	Aae04543 Pacific o
834	6	0.8	32	3	AY58650	Aay58650 Calluna v	907	6	0.8	44	2	AAAR42290	Aar42290 Peptatin
835	6	0.8	32	3	AA333972	Aay333972 Human sec	908	6	0.8	44	2	AAAR87212	Aar87212 Restin de
836	6	0.8	32	3	AA333972	Aay333972 Human sec	909	6	0.8	44	3	AAAB16864	Aab16864 Bacteriop
837	6	0.8	32	3	AA44807	Aay44807 Calluna v	910	6	0.8	44	3	AAAB53554	Aab53554 Human col
838	6	0.8	32	4	AA660746	Aab60746 Human sec	911	6	0.8	44	5	ADH32400	Adh32400 Yeast smo
839	6	0.8	33	2	AAAR80170	Aar80170 MiSP1-der	912	6	0.8	46	6	AAU90665	Aau90665 Human imm
840	6	0.8	33	4	AAAM16134	Aam16134 Peptide #	913	6	0.8	46	6	ABU00068	Abu00068 Human nov
841	6	0.8	33	4	AAAM28628	Aam28628 Peptide #	914	6	0.8	47	2	AAAR80176	Aar80176 MiSP1-der
842	6	0.8	33	4	AAAM83228	Aam83228 Human imm	915	6	0.8	47	2	AAAR80178	Aar80178 MiSP1-der
843	6	0.8	33	4	AAAB29945	Abb29945 Peptide #	916	6	0.8	48	2	AAAR80172	Aar80172 MiSP1-der
844	6	0.8	33	4	AAAM68319	Aam68319 Human bon	917	6	0.8	48	2	AAAO10583	Aao10583 Human pol
845	6	0.8	33	4	ABG49983	Abg49983 Human liv	918	6	0.8	48	7	ADA49395	Ada49395 Lymphaden
846	6	0.8	33	4	AAAM03864	Aam03864 Peptide #	919	6	0.8	49	2	AAAR80173	Aar80173 MiSP1-der
847	6	0.8	33	5	ABG77069	Abg77069 Prostate	920	6	0.8	49	3	AAAG12570	Aag12570 Zea may
848	6	0.8	33	5	ABG37869	Abg37869 Human pep	921	6	0.8	49	8	ADL97663	Adl97663 Protein e
849	6	0.8	33	5	ABO59958	Abo59958 Human gen	922	6	0.8	50	2	AAAR80179	Aar80179 MiSP1-der
850	6	0.8	34	2	AAAR45483	Aar45483 Parathyro	923	6	0.8	50	2	AAW89339	Aaw89339 Salmonell
851	6	0.8	34	2	AAAR80175	Aar80175 MiSP1-der	924	6	0.8	50	5	ABP06117	Abp06117 Human ORF
852	6	0.8	34	2	AAAR69009	Aar69009 PTH analo	925	6	0.8	50	7	ABM74476	Abm74476 DNA clone
853	6	0.8	34	2	AAW13300	Aaw13300 Truncated	926	6	0.8	51	2	AAAR80171	Aar80171 MiSP1-der
854	6	0.8	34	2	AAW12179	Aaw12179 Parathyro	927	6	0.8	51	2	AAAR80182	Aar80182 MiSP1-der
855	6	0.8	34	2	AAW61677	Aaw61677 Parathyro	928	6	0.8	51	4	ABBA2173	Abb42173 Peptide #
856	6	0.8	34	2	AAW65997	Aaw65997 Parathyro	929	6	0.8	51	4	ABBA2863	Abb42863 Peptide #
857	6	0.8	34	2	AAW81893	Aaw81893 Synthetic	930	6	0.8	51	4	AAAM35980	Aam35980 Peptide #
858	6	0.8	34	2	AAW74357	Aaw74357 Modified	931	6	0.8	51	4	AAAM36677	Aam36677 Peptide #
859	6	0.8	34	3	AAAB38530	Aab38530 Human sec	932	6	0.8	51	4	ABB26136	Abb26136 Protein #
860	6	0.8	34	5	AAU733134	Aau733134 Parathyro	933	6	0.8	51	4	AAW75869	Aam75869 Human bon
861	6	0.8	34	5	AAU733100	Aau733100 Parathyro	934	6	0.8	51	4	AAW76570	Aam76570 Human bon
862	6	0.8	34	5	AAU733101	Aau733101 Parathyro	935	6	0.8	51	4	AAW63756	Aam63756 Human bra
863	6	0.8	34	8	ABU42245	Abu42245 Protein e	936	6	0.8	51	4	AAAM63058	Aam63058 Human bra
864	6	0.8	34	8	ADH35573	Adh35573 Human par	937	6	0.8	51	4	ABG58269	Abg58269 Human liv
865	6	0.8	34	8	ADH35571	Adh35571 Human par	938	6	0.8	51	4	ABG57603	Abg57603 Human liv
866	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP	939	6	0.8	51	4	AAAG90451	Aag90451 C Glutami
867	6	0.8	34	8	ADQ75416	Adq75416 PTH/PTHrP	940	6	0.8	51	5	ABP02926	Abp02926 Human ORF
868	6	0.8	34	8	ADQ75449	Adq75449 PTH/PTHrP	941	6	0.8	51	5	ABG45818	Abg45818 Human pep
869	6	0.8	34	9	ABE51295	Aeb51295 Human PTH	942	6	0.8	52	3	ABG26169	Abg26169 Rat GBX2
870	6	0.8	34	9	ABE51293	Aeb51293 Human PTH	943	6	0.8	52	4	AAU86739	Aau86739 Novel hum
871	6	0.8	34	9	ABE70785	Aeb70785 Human PTH	944	6	0.8	52	4	AAU52328	Aau52328 Propionib
872	6	0.8	34	9	ABE70787	Aeb70787 Human PTH	945	6	0.8	52	6	ABM48847	Abm48847 Propionib
873	6	0.8	35	4	AAO13575	Aao13575 Human pol	946	6	0.8	52	7	ADB60073	Adb60073 Connectiv
874	6	0.8	36	2	AAAM58185	Aam58185 [Lys18]-h	947	6	0.8	52	8	ABO59052	Abo59052 Human gen
875	6	0.8	36	4	AAW15740	Aam15740 Peptide #	948	6	0.8	52	8	ADU02556	Adu02556 Novel hum
876	6	0.8	36	4	AAW28249	Aam28249 Peptide #	949	6	0.8	53	7	ADF59117	Adf59117 Human pol
877	6	0.8	36	4	ABE29559	Abb29559 Peptide #	950	6	0.8	54	3	AAAB34069	Aab34069 Human sec
878	6	0.8	36	4	ABE20152	Abb20152 Human bon	951	6	0.8	54	8	ABP08116	Abp08116 Human ORF
879	6	0.8	36	4	AAAM67923	Aam67923 Human bra	952	6	0.8	54	8	ADT38445	Adt38445 hSARS vir
880	6	0.8	36	4	ABG49566	Abg49566 Human liv	953	6	0.8	54	8	ADT38445	Adt38445 hSARS vir
881	6	0.8	36	4	ABG49566	Abg49566 Human liv	954	6	0.8	55	2	AAAR80177	Aar80177 MiSP1-der
882	6	0.8	36	4	AAW03474	Aam03474 Peptide #	955	6	0.8	55	4	ABBA3693	Abb43693 Peptide #
883	6	0.8	36	9	ABW94818	Aab94818 M. xanthu	956	6	0.8	55	4	AAAM82838	Aam82838 Human imm
884	6	0.8	37	4	AAE00729	Aae00729 Homeodoma	957	6	0.8	55	4	AAU40171	Aau40171 Propionib
885	6	0.8	37	4	AAAM14064	Aam14064 Peptide #	958	6	0.8	55	4	AAU52709	Aau52709 Propionib
886	6	0.8	38	4	ABB33009	Abb33009 Peptide #	959	6	0.8	55	4	ABG59065	Abg59065 Human liv
887	6	0.8	38	4	AAW26470	Aam26470 Peptide #	960	6	0.8	55	6	ABM36690	Abm36690 Propionib
888	6	0.8	38	4	ABB27838	Abb27838 Human pep	961	6	0.8	55	6	ABM49228	Abm49228 Propionib
889	6	0.8	38	4	ABBI8482	Abb18482 Protein #	962	6	0.8	55	6	ABM49228	Abm49228 Propionib
890	6	0.8	38	4	AAAM66193	Aam66193 Human bon	963	6	0.8	55	6	ABU56878	Abu56878 BoNT/A Hc
891	6	0.8	38	4	AAAM53807	Aam53807 Human bra	964	6	0.8	55	6	ABU56877	Abu56877 BoNT/A Hc
892	6	0.8	38	4	ABG47861	Abg47861 Human liv	965	6	0.8	56	2	AAW77572	Aaw77572 Staphyloc
893	6	0.8	38	4	AAW01804	Aam01804 Peptide #	966	6	0.8	56	3	AAAB33881	Aab33881 Human sec
894	6	0.8	38	5	ABG35843	Abg35843 Human pep	967	6	0.8	56	4	AAAM19289	Aam19289 Peptide #
895	6	0.8	38	8	ADN46506	Adn46506 Thermococ	968	6	0.8	56	4	ABB38566	Abb38566 Peptide #
896	6	0.8	39	2	AAAR80174	Aar80174 MiSP1-der	969	6	0.8	56	4	AAAM32017	Aam32017 Peptide #
897	6	0.8	39	3	AAAY55704	Aay55704 M. genita	970	6	0.8	56	4	ABB23694	Abb23694 Protein #
898	6	0.8	39	4	AAU21463	Aau21463 Human nov	971	6	0.8	56	4	AAW71725	Aam71725 Human bon
899	6	0.8	39	8	ABO56803	Abo56803 Human gen	972	6	0.8	56	4	AAO10744	Aao10744 Human pol
900	6	0.8	40	2	AAW85845	Aay85845 S. pneumo	973	6	0.8	56	4	AAAM59190	Aam59190 Human bra



974 6 0.8 56 4 ABG53410 Human liv  
975 6 0.8 56 5 ABP10151 Human ORF  
976 6 0.8 56 5 ABG41539 Human pep  
977 6 0.8 57 2 AAY12580 Human 5'  
978 6 0.8 57 4 AAM13734 Peptide #  
979 6 0.8 57 4 ABB32669 Peptide #  
980 6 0.8 57 4 AAM8987 Human imm  
981 6 0.8 57 4 ABG47522 Human liv  
982 6 0.8 58 4 AAB65135 Rat phys1  
983 6 0.8 58 4 AAM89036 Human imm  
984 6 0.8 58 4 AAU63871 Propionib  
985 6 0.8 58 4 ABG22198 Novel hum  
986 6 0.8 58 6 ABM60390 Propionib  
987 6 0.8 58 8 ADW15853 ADAMS55 e  
988 6 0.8 59 2 AAW26186 Fragment  
989 6 0.8 59 4 ABB69382 Drosophil  
990 6 0.8 59 4 ABB28297 Human pep  
991 6 0.8 59 4 AAM66647 Human bon  
992 6 0.8 59 4 AAO12589 Human pol  
993 6 0.8 59 4 AAU55699 Propionib  
994 6 0.8 59 4 AAM54254 Human bra  
995 6 0.8 59 6 ABM52218 Propionib  
996 6 0.8 60 2 AAY05924 Thermophi  
997 6 0.8 60 2 AAY45146 Rat ligam  
998 6 0.8 60 4 AAM16802 Peptide #  
999 6 0.8 60 4 AAB65132 Rat phys1  
1000 6 0.8 60 4 AAG74452 Human col

ALIGNMENTS

RESULT 1  
AAY84947  
XX AAY84947 standard; protein; 797 AA.  
AC AAY84947;  
XX  
DT 21-AUG-2000 (first entry)  
XX  
DE Amino acid sequence of outer membrane protein (omp) 85.  
XX  
KW Outer membrane protein; omp85; gonococcal infection; symptomatic disease;  
KW meningococcal infection; protective immune response; vaccine.  
XX  
OS Neisseria meningitidis.  
XX  
PN WO200023595-A1.  
XX  
PD 27-APR-2000.  
XX  
XX 22-OCT-1998; 98WO-US022352.  
XX  
XX 22-OCT-1998; 98WO-US022352.  
XX  
XX (UYMO-) UNIV MONTANA.  
XX  
XX Judd RC, Manning SD;  
XX  
XX WPI; 2000-339694/29.  
XX  
XX N-FSDB; AAA15156.  
XX  
XX New isolated outer membrane protein 85 of Neisseria gonorrhoeae and N.  
XX meningitidis useful for vaccine, therapeutic and diagnostic compositions  
XX for gonococcal or meningococcal infections.  
XX  
XX Claim 41; Page 89-92; 98pp; English.  
XX  
XX The present sequence represents an outer membrane protein (omp) 85 of  
XX Neisseria meningitidis. The omp polypeptides and polynucleotides are  
XX useful in compositions for use in the prevention, treatment and diagnosis  
XX of non-symptomatic gonococcal infection or meningococcal infection and  
XX symptomatic disease. They are also useful for the detection of

CC hybridisation complexes. Antigens and antibodies specific omp proteins  
CC also provide diagnostic, therapeutic and prophylactic compositions for  
CC the treatment or prevention of the infections described above. The  
CC antibodies are useful for inducing a protective immune response in humans  
CC or animals with N. gonorrhoeae, N. meningitidis, or other Neisseria  
CC species. The proteins, antibodies and polynucleotide sequences of the  
CC present invention may also be used in the screening and development of  
CC chemical compounds such as drugs or vaccines  
XX  
SQ Sequence 797 AA;

Query Match 100.0%; Score 797; DB 3; Length 797;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MKLKQIASALMLGISTPLAFADFTTQDIVERGLQRTPESTVFNLYLPVKVGDYNDTHGSA 60  
Db 1 MKLKQIASALMLGISTPLAFADFTTQDIVERGLQRTPESTVFNLYLPVKVGDYNDTHGSA 60  
Qy 61 IIKSLVATGFDDVRVETADGOLLTVIERPTIGSLNITGAKMLQNDAIKQLESFGLAQ 120  
Db 61 IIKSLVATGFDDVRVETADGOLLTVIERPTIGSLNITGAKMLQNDAIKQLESFGLAQ 120  
Qy 121 SQYFNQATLNQAVAGLKEEYLRGKLNIIQITPKVTKLARNRVDIDITIDEGKSAKITDIE 180  
Db 121 SQYFNQATLNQAVAGLKEEYLRGKLNIIQITPKVTKLARNRVDIDITIDEGKSAKITDIE 180  
Qy 181 FEGNQVYSRKLQRMSLTGEGGIWTLTRSNQFNEQFAQDMKEKVTDFQNNGYDFRIL 240  
Db 181 FEGNQVYSRKLQRMSLTGEGGIWTLTRSNQFNEQFAQDMKEKVTDFQNNGYDFRIL 240  
Qy 241 DTDIOTNEDKTQTIKITVHEGGRFWGKVSIEGDTNEVPKAELEKLLTWKPKWTERQQ 300  
Db 241 DTDIOTNEDKTQTIKITVHEGGRFWGKVSIEGDTNEVPKAELEKLLTWKPKWTERQQ 300  
Qy 301 MTAVLGEIQNRMGSAGYAYSEISVQPLPNAETKTVDVFLHIEPRKIYVNEIHTGNKT 360  
Db 301 MTAVLGEIQNRMGSAGYAYSEISVQPLPNAETKTVDVFLHIEPRKIYVNEIHTGNKT 360  
Qy 361 RDEVVRRELQRMESAPYDTSKLQSKVERVELLGYFDNVQFDAPVPLAGTDPKVDLNNSLTE 420  
Db 361 RDEVVRRELQRMESAPYDTSKLQSKVERVELLGYFDNVQFDAPVPLAGTDPKVDLNNSLTE 420  
Qy 421 RSTGSLDLSAGWQDTGLVMSAGVSQDNLFPGTGSAAALRASRKTTLNGSLSFDPYFTA 480  
Db 421 RSTGSLDLSAGWQDTGLVMSAGVSQDNLFPGTGSAAALRASRKTTLNGSLSFDPYFTA 480  
Qy 481 DGVSGLGYDVYKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540  
Db 481 DGVSGLGYDVYKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540  
Qy 541 YNKAPKHYADFIKKYKTDGTSFGKWLKGTGVGRNKTDLSALWPTRGYLTGVNAEIA 600  
Db 541 YNKAPKHYADFIKKYKTDGTSFGKWLKGTGVGRNKTDLSALWPTRGYLTGVNAEIA 600  
Qy 601 LPGSKLQYYSATHNQWTFEPPLSKITFTMLGGEVGIAGGYGRTKEIPFFENFYGGGLGSVR 660  
Db 601 LPGSKLQYYSATHNQWTFEPPLSKITFTMLGGEVGIAGGYGRTKEIPFFENFYGGGLGSVR 660  
Qy 661 GYESGTLGPKVYDEYGEKISYGGNKANVSAAELFFPMPGAADARTVRLSLFADAGSVWDG 720  
Db 661 GYESGTLGPKVYDEYGEKISYGGNKANVSAAELFFPMPGAADARTVRLSLFADAGSVWDG 720  
Qy 721 KTYDDNSSSSATGGRVQNIYAGANTHKSFTTNELRYSGAGVATWLSPLGPMKFRYAYPLKK 780  
Db 721 KTYDDNSSSSATGGRVQNIYAGANTHKSFTTNELRYSGAGVATWLSPLGPMKFRYAYPLKK 780  
Qy 781 KPDEIQRFOFQLGTTTF 797  
Db 781 KPDEIQRFOFQLGTTTF 797

RESULT 2



```

ABR79802
ID ABR79802 standard; protein; 797 AA.
XX AC
XX AB79802;
XX DT
XX 15-NOV-2002 (first entry)
XX DE
XX Neisseria meningitidis outer membrane protein Omp85.
XX KW
XX Outer membrane protein; Omp85; meningitis; vaccine; diagnosis;
XX OS antibacterial.
XX FH
XX Neisseria meningitidis.
XX FT
XX Key Location/Qualifiers
XX Peptide 1..21
XX Protein /label= Signal_peptide
XX FT 22..797
XX FT /label= Mature_protein
XX PN US2002086028-A1.
XX PD
XX 04-JUL-2002.
XX PF 26-NOV-2001; 2001US-00994192.
XX PR 22-OCT-1998; 98US-00177039.
XX PA (JUDD/) JUDD R C.
XX PA (MANN/) MANNING D S.
XX PI
XX Judd RC, Manning DS;
XX PI WPI; 2002-642234/69.
XX DR
XX Novel immunogenic composition for vaccinating against meningococcal or
XX PT gonococcal infection, comprises Omp85 protein of Neisseria meningitidis
XX PT or Neisseria gonorrhoeae, or nucleic acid encoding the protein.
XX PS
XX Claim 13; Fig 5; 30pp; English.
XX CC
XX The present sequence is that of the Neisseria meningitidis strain HH
XX CC outer membrane protein 85 (Omp85), as predicted from a gene that was
XX CC obtained from a genomic DNA by PCR amplification using primers based
XX CC on the gonococcal Omp85 gene. The meningococcal Omp85 protein is 95%
XX CC identical and 98% similar to gonococcal Omp85 (see ABB79801). Claimed
XX CC immunogenic compositions comprise N. meningitidis Omp85, its fragments,
XX CC fusion proteins including the Omp85, or nucleic acids encoding them,
XX CC which induce a protective immune response in a subject. The immunogenic
XX CC compositions may also include an antigen from a heterologous or
XX CC homologous pathogen, or a nucleic acid encoding it. They are used in a
XX CC claimed method of vaccinating a human or animal against non-symptomatic
XX CC meningococcal infection or symptomatic disease. A kit for diagnosing
XX CC infection with N. meningitidis comprising labelled Omp85 is also claimed.
XX CC The Omp85 polypeptides and polynucleotides are also useful in drug
XX CC screening and development
XX CC
XX SQ Sequence 797 AA;
XX
Query Match 100.0%; Score 797; DB 5; Length 797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKLQIASALMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
DB 1 MKLQIASALMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
QY 61 IIKSLYATGFDDRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKXLESFGLAQ 120
DB 61 IIKSLYATGFDDRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKXLESFGLAQ 120
QY 121 SQYFNQATLNQAVAGLKEEYLGKLNIOITPKVTKLARNRVDIDITIDEGKSAKITDIE 180
DB 121 SQYFNQATLNQAVAGLKEEYLGKLNIOITPKVTKLARNRVDIDITIDEGKSAKITDIE 180
QY 181 FEQNOVYSRDKLMRQMSLTGEGGIWTLTRSNQFNEQKFAQDMKEKVTDFYQNNGYFDFRIL 240
DB 181 FEQNOVYSRDKLMRQMSLTGEGGIWTLTRSNQFNEQKFAQDMKEKVTDFYQNNGYFDFRIL 240
QY 241 DTDIOTNEDKTQTIKITHHEGGRFRWGVKVISIEGDTNEVPKAELEKLLTKPKGWYERQQ 300
DB 241 DTDIOTNEDKTQTIKITHHEGGRFRWGVKVISIEGDTNEVPKAELEKLLTKPKGWYERQQ 300
QY 301 MTAVLGEIQNRMGSAQYAYSEISVQPLPNAETKTDFVLHIEPGRKIYVNEIHTGNKKT 360
DB 301 MTAVLGEIQNRMGSAQYAYSEISVQPLPNAETKTDFVLHIEPGRKIYVNEIHTGNKKT 360
QY 361 RDEVVRELQRMESAPYDTSKLRKSERVELLYGFDNVQFDPVPLACTPKVDLNMSLTE 420
DB 361 RDEVVRELQRMESAPYDTSKLRKSERVELLYGFDNVQFDPVPLACTPKVDLNMSLTE 420
QY 421 RSTGSLDLSAGWQDTGLVMSAGVSQDNLFCTGKSAALRASRSKTTLNGSLSFDPYFTA 480
DB 421 RSTGSLDLSAGWQDTGLVMSAGVSQDNLFCTGKSAALRASRSKTTLNGSLSFDPYFTA 480
QY 481 DGVSLGYDVYKAFDPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
DB 481 DGVSLGYDVYKAFDPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
QY 541 YNKAPKHADFIKKYKTDGTSFGKWLKGTGVRNKTDSALWPTRGYLTGVNAEIA 600
DB 541 YNKAPKHADFIKKYKTDGTSFGKWLKGTGVRNKTDSALWPTRGYLTGVNAEIA 600
QY 601 LPSKLOYSATHNQWTFPLSKTFTLMLGGEVGIAGGYGRTKEIPFFENFYGGGLGSVR 660
DB 601 LPSKLOYSATHNQWTFPLSKTFTLMLGGEVGIAGGYGRTKEIPFFENFYGGGLGSVR 660
QY 661 GYESGTLGPKYDYEYGEKISYGGNKKANVSALLFPMPGAQDAETVRLSLFADAGSVWDG 720
DB 661 GYESGTLGPKYDYEYGEKISYGGNKKANVSALLFPMPGAQDAETVRLSLFADAGSVWDG 720
QY 721 KTYDDNSSATGGRVQNIYGAGNTHKSTFTNELYSGAGGAVTWLSPLGPMKFRYAYPLKK 780
DB 721 KTYDDNSSATGGRVQNIYGAGNTHKSTFTNELYSGAGGAVTWLSPLGPMKFRYAYPLKK 780
QY 781 KPEDEIQRFQFQLGTTTF 797
DB 781 KPEDEIQRFQFQLGTTTF 797
RESULT 3
ADZ09417
ID ADZ09417 standard; protein; 797 AA.
XX AC ADZ09417;
XX DT 16-JUN-2005 (first entry)
XX DE Neisseria meningitidis outer membrane protein Omp85.
XX KW outer membrane protein; Omp85; antibacterial; vaccine; infection.
XX OS Neisseria meningitidis.
XX PN US2005074458-A1.
XX PD 07-APR-2005.
XX PF 26-JUN-2003; 2003US-00606618.
XX PR 22-OCT-1998; 98US-00177039.
XX PR 26-NOV-2001; 2001US-00994192.
XX PA (UYMO-) UNIV MONTANA.
XX PI Judd RC, Manning DS;

```

XX  
DR WPI; 2005-272369/28.  
DR N-PSDB; ADZ09416.  
XX  
PT New isolated nucleic acid encoding outer membrane protein 85 (Omp85) of  
PT Neisseria gonorrhoeae or Neisseria meningitidis, useful for preventing,  
PT treating, or diagnosing non-symptomatic gonococcal infection or  
PT meningococcal infection.  
XX  
PS Claim 1; SEQ ID NO 4; 41bp; English.  
XX  
CC The invention relates to a nucleic acid molecule comprising: (a) the 2379  
CC or 2394 bp sequence of ADZ09414 or ADZ09416; or (b) a sequence capable of  
CC hybridizing to it, or its fragment, which when expressed in a host cell  
CC produces the outer membrane protein Omp85 polypeptide which induces  
CC antibodies to Neisseria gonorrhoeae or N. meningitidis, under the control  
CC of suitable regulatory sequences which direct expression of the  
CC polypeptide in the host cell. The nucleic acid and amino acid sequences  
CC of the Omp85 protein of N. gonorrhoeae or N. meningitidis are useful as  
CC vaccine compositions, therapeutic compositions, and diagnostic  
CC compositions for preventing, treating, or diagnosing non-symptomatic  
CC gonococcal infection or symptomatic disease and non-symptomatic  
CC meningococcal infection and symptomatic disease. The present sequence  
CC represents the N. meningitidis Omp85 protein. Note: the N. meningitidis  
CC Omp85 protein is referred to the Genbank accession number AF021045, but  
CC this number refers to the *Oncorhynchus kisutch* insulin-like growth factor  
CC receptor-2 (SIR-6) mRNA, partial cds sequence.  
XX  
SQ Sequence 797 AA;  
  
Query Match 100.0%; Score 797; DB 9; Length 797;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 MKLQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDTYNDTHGSA 60  
Db 1 MKLQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDTYNDTHGSA 60  
  
Qy 61 IIKSLYATGFFDVRVETADQQLLTIVIERPTIGSLNITGAKMLQNDIAIKNLESFGLAQ 120  
Db 61 IIKSLYATGFFDVRVETADQQLLTIVIERPTIGSLNITGAKMLQNDIAIKNLESFGLAQ 120  
  
Qy 121 SOYENQATLNOAVAGLKEEYLGKLNIOITPKVTKLARNRVIDITIDEGSKAKITDIE 180  
Db 121 SOYFNQATLNOAVAGLKEEYLGKLNIOITPKVTKLARNRVIDITIDEGSKAKITDIE 180  
  
Qy 181 FEGNQVYSDRKLQMQLSITEGGIWTWLTNRNQFNEQKFAQDMKVTFDYQNGYDFDPRIL 240  
Db 181 FEGNQVYSDRKLQMQLSITEGGIWTWLTNRNQFNEQKFAQDMKVTFDYQNGYDFDPRIL 240  
  
Qy 241 DTDIQTWEDTKQITKITVHEGGRFRGKVSIEGDTNEVPKAELEKLLTWKPGKWERQQ 300  
Db 241 DTDIQTWEDTKQITKITVHEGGRFRGKVSIEGDTNEVPKAELEKLLTWKPGKWERQQ 300  
  
Qy 301 MTAVLGIIQNRMSGAYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKT 360  
Db 301 MTAVLGIIQNRMSGAYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKT 360  
  
Qy 361 RDEVVRELROMESAPYDTSKLQSKERVLLGVDFNVQFQDAVPLAGTDPKVDLNMSLTE 420  
Db 361 RDEVVRELROMESAPYDTSKLQSKERVLLGVDFNVQFQDAVPLAGTDPKVDLNMSLTE 420  
  
Qy 421 RSTGSLDLSAGWQDGTGLVMSAGVSDNLFTGTGSAALRASRSKTTLNGSLSFDPYFTA 480  
Db 421 RSTGSLDLSAGWQDGTGLVMSAGVSDNLFTGTGSAALRASRSKTTLNGSLSFDPYFTA 480  
  
Qy 481 DGVS LGDVGVCAPDPKASTSIKQYKTTTAGAGIRMSVPVTEYDRNFGVLAHFLVNT 540  
Db 481 DGVS LGDVGVCAPDPKASTSIKQYKTTTAGAGIRMSVPVTEYDRNFGVLAHFLVNT 540  
  
Qy 541 YNKAPKHVADFIKKYKGTGDTGDSFGKWLKYGTGVGGRNKTDLSALWTRGYLTGVNAEIA 600  
Db 541 YNKAPKHVADFIKKYKGTGDTGDSFGKWLKYGTGVGGRNKTDLSALWTRGYLTGVNAEIA 600

Qy 601 LPQSKLOYYSATHNOTWFFPLSKTFTMLGSGEVGIAGGYGRTKEIIPFFSNFYGGGLGSVR 660  
Db 601 LPQSKLOYYSATHNOTWFFPLSKTFTMLGSGEVGIAGGYGRTKEIIPFFSNFYGGGLGSVR 660  
  
Qy 661 GYESGTLGPKVYDEYGEKISYGNKKANYSALLFPMPGAKDARTVRLSLFADAGSVWDG 720  
Db 661 GYESGTLGPKVYDEYGEKISYGNKKANYSALLFPMPGAKDARTVRLSLFADAGSVWDG 720  
  
Qy 721 KTYDDNSSATGGRVONIYGAGNTHKSTFTNLRYSAGGAVTWLSPLGPMKFRYAYPLKK 780  
Db 721 KTYDDNSSATGGRVONIYGAGNTHKSTFTNLRYSAGGAVTWLSPLGPMKFRYAYPLKK 780  
  
Qy 781 KPEDEIQRFOFQLGTTTF 797  
Db 781 KPEDEIQRFOFQLGTTTF 797  
  
RESULT 4  
AAU03959  
ID AAU03959 standard; protein; 797 AA.  
XX  
AC AAU03959;  
XX  
DT 23-OCT-2001 (first entry)  
XX  
DE Neisseria gonorrhoeae antigenic protein.  
XX  
KW Antigenic protein; pharynx; meningitis; septicaemia; mammalian cell;  
KW bacterial infection; baculovirus; yeast; Neisseria meningitidis.  
XX  
OS Neisseria gonorrhoeae.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..21 /note= "Signal peptide"  
FT Protein 22..797  
FT /note= "Mature N. gonorrhoeae antigen"  
XX  
PN WO200138350-A2.  
XX  
PD 31-MAY-2001.  
XX  
PF 28-NOV-2000; 2000WO-IB001851.  
XX  
PR 29-NOV-1999; 99GB-00028197.  
PR 09-MAR-2000; 2000GB-00005698.  
XX  
PA (CHIR-) CHIRON SPA.  
PA (STAT-) STATENS INST FOLKEHELSE.  
XX  
PI Giuliani MM, Pizza M, Rappuoli R, Holst J;  
XX  
DR WPI; 2001-381289/40.  
DR N-PSDB; AAS07279.  
XX  
DR Novel 85 kDa antigen from Neisseria meningitidis and Neisseria  
PT gonorrhoeae, useful in the manufacture of a medicament for treating and  
PT preventing Neisserial bacteria infection.  
XX  
PS Claim 1; Page 37-39; 92pp; English.  
XX  
CC The sequence represents a Neisseria gonorrhoeae 85 kDa antigenic protein.  
CC N. gonorrhoeae is closely related to N. meningitidis, which colonises the  
CC pharynx, causing meningitis and, occasionally, septicaemia in the absence  
CC of meningitis. This antigenic protein is useful in the manufacture of a  
CC medicament for treating or preventing infection due to Neisseria  
CC bacteria, such as meningitis and septicaemia. It is also useful as a  
CC diagnostic reagent for detecting the presence of Neisseria bacteria or  
CC antibodies raised against Neisseria, and as a reagent for raising the  
CC antibodies. The Neisserial nucleotide sequences can be expressed in a  
CC variety of different expression systems, for example, mammalian cells,  
CC baculoviruses, plants, bacteria and yeast

XX	SQ	Sequence	797 AA;
		Query Match	94.4%; Score 752; DB 4; Length 797;
		Best Local Similarity	100.0%; Pred. No. 0;
		Matches 752; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	21	ADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSALIKSLYATGFPDDVRVETAD	80
DB	21	ADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSALIKSLYATGFPDDVRVETAD	80
QY	81	GQLLLTVIERPTTIGSLNITGAKMLONDAIKNLESFGLAQSOYFNOATLNOAVAGLKEEY	140
DB	81	GQLLLTVIERPTTIGSLNITGAKMLONDAIKNLESFGLAQSOYFNOATLNOAVAGLKEEY	140
QY	141	LGRGKLNIOQTPKVKTKLARNRVDIDITIDEGKSAKITDIEPEGNQVYSDRKLQMSLITE	200
DB	141	LGRGKLNIOQTPKVKTKLARNRVDIDITIDEGKSAKITDIEPEGNQVYSDRKLQMSLITE	200
QY	201	GGFTWLTRSNQFNEQKFAQDMEKVTFYQNNGYFDFRILDTDITQNEDEKTKQIKITVH	260
DB	201	GGFTWLTRSNQFNEQKFAQDMEKVTFYQNNGYFDFRILDTDITQNEDEKTKQIKITVH	260
QY	261	EGGRFRNGKVISIEGDTNEVPKAELEKLLTMKPGKMYERQOMTAVLGEIQNRMGSGAYVS	320
DB	261	EGGRFRNGKVISIEGDTNEVPKAELEKLLTMKPGKMYERQOMTAVLGEIQNRMGSGAYVS	320
QY	321	EISVQPLPNAETKTVDFVLHIIEPGRKIVVNEIHITGNKTRDEVVRELRLQMESAPYDTS	380
DB	321	EISVQPLPNAETKTVDFVLHIIEPGRKIVVNEIHITGNKTRDEVVRELRLQMESAPYDTS	380
QY	381	KLQSKERVEVLGYFDNVQFQDAVPLAGTPDKVDLNMSLTERSTGSLDLSAGWQDTGLVM	440
DB	381	KLQSKERVEVLGYFDNVQFQDAVPLAGTPDKVDLNMSLTERSTGSLDLSAGWQDTGLVM	440
QY	441	SAGVSQNLFGTGKSAALRASRKTTLNGSLSPFTDPTADGVSLGYDVGKAFDPRKAS	500
DB	441	SAGVSQNLFGTGKSAALRASRKTTLNGSLSPFTDPTADGVSLGYDVGKAFDPRKAS	500
QY	501	TSIKOYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNAKPKHVADFIKKYKTKDG	560
DB	501	TSIKOYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNAKPKHVADFIKKYKTKDG	560
QY	561	TGDSFKGLYKGTGWMGRNKDTSALWPTRGYLTGVNAEIALPGSKLOYYSATHNQTFWFP	620
DB	561	TGDSFKGLYKGTGWMGRNKDTSALWPTRGYLTGVNAEIALPGSKLOYYSATHNQTFWFP	620
QY	621	LSKTFPTLMGGEVGIAGGYGRTKETIPPTENFYGGGLGSRVGYESGTGPKVYDEYGEKIS	680
DB	621	LSKTFPTLMGGEVGIAGGYGRTKETIPPTENFYGGGLGSRVGYESGTGPKVYDEYGEKIS	680
QY	681	YGGNKKANVSARELLPMPGAKDARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIYG	740
DB	681	YGGNKKANVSARELLPMPGAKDARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIYG	740
QY	741	AGNTHKSTFTNELRYSAGGAVTWLSPLGPMKF	772
DB	741	AGNTHKSTFTNELRYSAGGAVTWLSPLGPMKF	772
RESULT 5			
AAU03957			
ID	AAU03957 standard; protein; 797 AA.		
XX	AAU03957;		
AC	AAU03957;		
XX	23-OCT-2001 (first entry)		
DT			
XX	Neisseria meningitidis serogroup B antigenic protein.		
XX	Serogroup B antigen; pharynx; meningitis; septicaemia; mammalian cell;		
KW	bacterial infection; baculovirus; yeast.		
XX			

Db 321 EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHITGNKTRDEVVRRELQMESAPYDTS 380  
Qy 381 KLQSKERVLLGYFDNVQFADVPLAGTDPKVDLNNLSLTERSTGSLDLSAGWQDTGLVM 440  
Db 381 KLQSKERVLLGYFDNVQFADVPLAGTDPKVDLNNLSLTERSTGSLDLSAGWQDTGLVM 440  
Qy 441 SAGVSQDNLFGTGKSAALRASRSKTTLNGSLSTDPYFTADGVSGLGVYDVYVKAFDPRKAS 500  
Db 441 SAGVSQDNLFGTGKSAALRASRSKTTLNGSLSTDPYFTADGVSGLGVYDVYVKAFDPRKAS 500  
Qy 501 TSISKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYKNKAPKHADFIKKYKTDG 560  
Db 501 TSISKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYKNKAPKHADFIKKYKTDG 560  
Qy 561 TDGSFKGWLYKGTGVGWRNKTTDSALWPTRGYLTGVNAEIALPGSKLQYYSATHNQWTFPP 620  
Db 561 TDGSFKGWLYKGTGVGWRNKTTDSALWPTRGYLTGVNAEIALPGSKLQYYSATHNQWTFPP 620  
Qy 621 LSKTFTLMLGGEVGIAGGYGRKTEIPFFENFYGGGLGSRVGYESGTLGPKVYDEYGEKIS 680  
Db 621 LSKTFTLMLGGEVGIAGGYGRKTEIPFFENFYGGGLGSRVGYESGTLGPKVYDEYGEKIS 680  
Qy 681 YGGNKKANVSAELLFPMPGAKDARTVRLSLFADAGSVWDGKTYDDNSSSATGGRVQNIY 740  
Db 681 YGGNKKANVSAELLFPMPGAKDARTVRLSLFADAGSVWDGKTYDDNSSSATGGRVQNIY 740  
Qy 741 AGNTHKSTFTNELRYSAGGAVTWLSPGLPMKF 772  
Db 741 AGNTHKSTFTNELRYSAGGAVTWLSPGLPMKF 772

RESULT 6

AAU04451  
ID AAU04451 standard; protein; 797 AA.  
XX AC AAU04451;  
XX 23-OCT-2001 (first entry)  
DE Neisseria meningitidis serogroup A antigenic protein #2.  
KW Serogroup B antigen; pharynx; meningitis; septicaemia; mammalian cell;  
KW bacterial infection; baculovirus; yeast.  
XX Neisseria meningitidis.  
Key Location/Qualifiers  
FH Peptide 1..21  
FT /note= "Signal peptide"  
FT Protein 22..797  
XX /note= "Mature N. meningitidis serogroup A antigen"  
XX WO200138350-A2.  
XX 31-MAY-2001.  
XX 28-NOV-2000; 2000WO-IB001851.  
XX 29-NOV-1999; 99GB-00028197.  
XX 09-MAR-2000; 2000GB-00005698.  
XX (CHIR-) CHIRON SPA.  
XX (STAT-) STATENS INST FOLKHELTSE.  
XX Giuliani MM, Pizza M, Rappuoli R, Holst J;  
XX WPI; 2001-381289/40.  
XX Novel 85 kDa antigen from Neisseria meningitidis and Neisseria  
XX gonorrhoeae, useful in the manufacture of a medicament for treating and  
XX preventing Neisserial bacteria infection.  
XX Claim 1; Page 39-40; 92pp; English.

XX The sequence represents a Neisseria meningitidis serogroup A 85 kDa  
CC antigenic protein. Neisseria meningitidis colonises the pharynx, causing  
CC meningitis and, occasionally, septicaemia in the absence of meningitis.  
CC This antigenic protein is useful in the manufacture of a medicament for  
CC treating or preventing infection due to Neisseria bacteria, such as  
CC meningitis and septicaemia. It is also useful as a diagnostic reagent for  
CC detecting the presence of Neisseria bacteria or antibodies raised against  
CC Neisseria, and as a reagent for raising the antibodies. The Neisserial  
CC nucleotide sequences can be expressed in a variety of different  
CC expression systems, for example, mammalian cells, baculoviruses, plants,  
CC bacteria and yeast. Note: There are two versions of this sequence  
CC displayed in the specification (see AAU03958)  
XX  
SQ Sequence 797 AA;  
Query Match 94.4%; Score 752; DB 4; Length 797;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 21 ADFTIODIRVEGLQRTPESTVFNYPVKVGDYNTDTHGSAIIKSLYATGFFDDVRVETAD 80  
Db 21 ADFTIODIRVEGLQRTPESTVFNYPVKVGDYNTDTHGSAIIKSLYATGFFDDVRVETAD 80  
Qy 81 GOLLTVIERPTIGSLNITGAKMLQNDALKNLESFGLAQSOYFNOATLNOAVAGLKEEY 140  
Db 81 GOLLTVIERPTIGSLNITGAKMLQNDALKNLESFGLAQSOYFNOATLNOAVAGLKEEY 140  
Qy 141 LGRGKLNIIQITPKVTKLARNRVDIDITIDEGKSAKITDIEFEGNQYVSDRKLQRMSLSTE 200  
Db 141 LGRGKLNIIQITPKVTKLARNRVDIDITIDEGKSAKITDIEFEGNQYVSDRKLQRMSLSTE 200  
Qy 201 GGIWTLTRSNQFNEQKPAQDMKVTDFYQNGNGYDFRILDTDIQNEDEKTKQTIKITH 260  
Db 201 GGIWTLTRSNQFNEQKPAQDMKVTDFYQNGNGYDFRILDTDIQNEDEKTKQTIKITH 260  
Qy 261 EGGRFPMGKVSIEGDTNEVPKAELEKLLTMKPGKYEROQMTAVLGEIQNRMGSAAYAS 320  
Db 261 EGGRFPMGKVSIEGDTNEVPKAELEKLLTMKPGKYEROQMTAVLGEIQNRMGSAAYAS 320  
Qy 321 EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHITGNKTRDEVVRRELQMESAPYDTS 380  
Db 321 EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHITGNKTRDEVVRRELQMESAPYDTS 380  
Qy 381 KLQSKERVLLGYFDNVQFADVPLAGTDPKVDLNNLSLTERSTGSLDLSAGWQDTGLVM 440  
Db 381 KLQSKERVLLGYFDNVQFADVPLAGTDPKVDLNNLSLTERSTGSLDLSAGWQDTGLVM 440  
Qy 441 SAGVSQDNLFGTGKSAALRASRSKTTLNGSLSTDPYFTADGVSGLGVYDVYVKAFDPRKAS 500  
Db 441 SAGVSQDNLFGTGKSAALRASRSKTTLNGSLSTDPYFTADGVSGLGVYDVYVKAFDPRKAS 500  
Qy 501 TSISKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYKNKAPKHADFIKKYKTDG 560  
Db 501 TSISKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYKNKAPKHADFIKKYKTDG 560  
Qy 561 TDGSFKGWLYKGTGVGWRNKTTDSALWPTRGYLTGVNAEIALPGSKLQYYSATHNQWTFPP 620  
Db 561 TDGSFKGWLYKGTGVGWRNKTTDSALWPTRGYLTGVNAEIALPGSKLQYYSATHNQWTFPP 620  
Qy 621 LSKTFTLMLGGEVGIAGGYGRKTEIPFFENFYGGGLGSRVGYESGTLGPKVYDEYGEKIS 680  
Db 621 LSKTFTLMLGGEVGIAGGYGRKTEIPFFENFYGGGLGSRVGYESGTLGPKVYDEYGEKIS 680  
Qy 681 YGGNKKANVSAELLFPMPGAKDARTVRLSLFADAGSVWDGKTYDDNSSSATGGRVQNIY 740  
Db 681 YGGNKKANVSAELLFPMPGAKDARTVRLSLFADAGSVWDGKTYDDNSSSATGGRVQNIY 740  
Qy 741 AGNTHKSTFTNELRYSAGGAVTWLSPGLPMKF 772  
Db 741 AGNTHKSTFTNELRYSAGGAVTWLSPGLPMKF 772

RESULT 7	
AAB23788	261 EGGFRFWGKVSIEGDTNEVPKAELEKLLTMKPGKTYERQOMTAVLGEIQNRMSAGYAYS 320
ID AAB23788 standard; protein; 797 AA.	261 EGGFRFWGKVSIEGDTNEVPKAELEKLLTMKPGKTYERQOMTAVLGEIQNRMSAGYAYS 320
XX	
AC AAB23788;	
XX	
12-JAN-2001 (first entry)	
DE Neisseria meningitidis serogroup A amino acid sequence.	
XX	
CG motif; complete Freund's adjuvant; phosphorothioate; immunogenic;	
XX	
Neisseria antigen; Neisseria meningitidis; Neisseria gonorrhoeae;	
XX	
bactericidal; antibacterial; vaccine; immunostimulatory; infection;	
XX	
immune response.	
XX	
Neisseria meningitidis.	
OS	
WO200050075-A2.	
PN	
31-AUG-2000.	
FD	
09-FEB-2000; 2000WO-IB000176.	
XX	
26-FEB-1999; 99US-0121792P.	
XX	
(CHIR-) CHIRON SPA.	
PA	
Grandi G, Rappuoli R, Giuliani MM, Pizza M;	
PI	
WPI; 2001-015529/02.	
XX	
Immunogenic composition useful for stimulating an immune response in a	
PT	
mammal against Neisseria infection, comprises Neisseria antigen and an	
PT	
adjuvant composition comprising an oligonucleotide with a CG motif.	
XX	
Claim 22; Page 33; 39pp; English.	
XX	
The present invention describes an immunogenic composition (I) comprising	
CC	
a Neisseria antigen and an adjuvant composition comprising an	
CC	
oligonucleotide comprising at least 1 CG motif. Also described is an	
CC	
adjuvant composition (II) comprising an oligonucleotide which comprises	
CC	
at least 1 CG motif and a complete Freund's adjuvant (CFA), where the	
CC	
oligonucleotide preferably comprises at least one phosphorothioate bond.	
CC	
AAA92359 to AAA92385 represent specifically claimed oligonucleotides of	
CC	
the present invention. (I) is useful for stimulating an immune response	
CC	
in a mammal, preferably a human, against Neisseria infection, preferably	
CC	
Neisseria meningitidis infection and in the manufacture of a medicament	
CC	
for inducing a protective immune response in a mammal. The present	
CC	
sequence represents the claimed Neisseria meningitidis serogroup A amino	
CC	
acid sequence disclosed in GB-9928197.4, which is given in the present	
CC	
invention	
XX	
SQ Sequence 797 AA;	
Query Match 94.4%; Score 752; DB 4; Length 797;	
Best Local Similarity 100.0%; Pred. NO. 0;	
Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 21 ADFTTQDIRVEGLQRTPESTVFNYPVKVGDYNDTHGSAIKSLYATGFFDDVRVETAD 80	
DB 21 ADFTTQDIRVEGLQRTPESTVFNYPVKVGDYNDTHGSAIKSLYATGFFDDVRVETAD 80	
QY 81 GQLLTIVIERPTIGSLNITGAKMLQNDATKKNLESGLAQSQYFNOATLNQAVAGKBEY 140	
DB 81 GQLLTIVIERPTIGSLNITGAKMLQNDATKKNLESGLAQSQYFNOATLNQAVAGKBEY 140	
QY 141 LGRGKLNIOITPKVTKLARNRVDITIDEGSAKITDIEFGNQVYSDRKLQMSLQTE 200	
DB 141 LGRGKLNIOITPKVTKLARNRVDITIDEGSAKITDIEFGNQVYSDRKLQMSLQTE 200	
QY 201 GGIWTWLTNSQNFQEKPAQDMKVTDFYQNGYFDFRLDITDQTNEDKTKQTIKIVH 260	
DB 201 GGIWTWLTNSQNFQEKPAQDMKVTDFYQNGYFDFRLDITDQTNEDKTKQTIKIVH 260	

QY	261	EGGFRFWGKVSIEGDTNEVPKAELEKLLTMKPGKTYERQOMTAVLGEIQNRMSAGYAYS	320
DB	261	EGGFRFWGKVSIEGDTNEVPKAELEKLLTMKPGKTYERQOMTAVLGEIQNRMSAGYAYS	320
QY	321	EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHIITGNKTRDEVVRELQMESAPYDTS	380
DB	321	EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHIITGNKTRDEVVRELQMESAPYDTS	380
QY	381	KLORSKERVLLCGYFONVQFDVPLAGTDPKVDLNMSLTERSTGSLDLSAGWQDTGLVM	440
DB	381	KLORSKERVLLCGYFONVQFDVPLAGTDPKVDLNMSLTERSTGSLDLSAGWQDTGLVM	440
QY	441	SAGVSQDNLFEGTGKSAALRASRSKTTLNGSLSTFDPYFTADGVSGLGYDVYKGFDPKPKAS	500
DB	441	SAGVSQDNLFEGTGKSAALRASRSKTTLNGSLSTFDPYFTADGVSGLGYDVYKGFDPKPKAS	500
QY	501	TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYKAPKHYADFIKKYKGTG	560
DB	501	TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYKAPKHYADFIKKYKGTG	560
QY	561	TDGSFKGWLKGTGVRGRNKTDSALWPTTRCYLTCVNAEIALPGSKLOYYSATHNQWFFP	620
DB	561	TDGSFKGWLKGTGVRGRNKTDSALWPTTRCYLTCVNAEIALPGSKLOYYSATHNQWFFP	620
QY	621	LSKTFTLMLGGEVGIAGGYGRTKEIPFFENFYGGGLSVRGYBSGTLGPKYDYDEYGEKIS	680
DB	621	LSKTFTLMLGGEVGIAGGYGRTKEIPFFENFYGGGLSVRGYBSGTLGPKYDYDEYGEKIS	680
QY	681	YGGNKKANVSAELLFPMGAKDARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIYG	740
DB	681	YGGNKKANVSAELLFPMGAKDARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIYG	740
QY	741	AGNTHKSTFTNELRYSAGGAVTWLSPLGPMKF	772
DB	741	AGNTHKSTFTNELRYSAGGAVTWLSPLGPMKF	772

RESULT 8

AAB23784

ID AAB23784 standard; protein; 797 AA.

XX

AC AAB23784;

XX

12-JAN-2001 (first entry)

DE Neisseria meningitidis serogroup B amino acid sequence.

XX

CG motif; complete Freund's adjuvant; phosphorothioate; immunogenic;

XX

Neisseria antigen; Neisseria meningitidis; Neisseria gonorrhoeae;

XX

bactericidal; antibacterial; vaccine; immunostimulatory; infection;

XX

immune response.

XX

Neisseria meningitidis.

OS

WO200050075-A2.

PN

31-AUG-2000.

PD

09-FEB-2000; 2000WO-IB000176.

PF

26-FEB-1999; 99US-0121792P.

PR

(CHIR-) CHIRON SPA.

PA

Grandi G, Rappuoli R, Giuliani MM, Pizza M;

PI

WPI; 2001-015529/02.

DR

Immunogenic composition useful for stimulating an immune response in a

PT

mammal against Neisseria infection, comprises Neisseria antigen and an

PT

adjuvant composition comprising an oligonucleotide with a CG motif.

XX

PS	Claim 22; Page 32; 39pp; English.	
XX		
CC	The present invention describes an immunogenic composition (I) comprising	
CC	a Neisseria antigen and an adjuvant composition comprising an	
CC	oligonucleotide comprising at least 1 CG motif. Also described is an	
CC	adjuvant composition (II) comprising an oligonucleotide which comprises	
CC	at least 1 CG motif and a complete Freund's adjuvant (CFA), where the	
CC	oligonucleotide preferably comprises at least one phosphorothioate bond.	
CC	AAA92359 to AAA92385 represent specifically claimed oligonucleotides of	
CC	the present invention. (I) is useful for stimulating an immune response	
CC	in a mammal, preferably a human, against Neisseria infection, preferably	
CC	Neisseria meningitidis infection and in the manufacture of a medicament	
CC	for inducing a protective immune response in a mammal. The present	
CC	sequence represents the claimed Neisseria meningitidis serogroup B amino	
CC	acid sequence disclosed in GB-9928197.4, which is given in the present	
CC	invention	
XX		
SQ	Sequence 797 AA;	
	Query Match 94.4%; Score 752; DB 4; Length 797;	
	Best Local Similarity 100.0%; Pred. No. 0;	
	Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	21 ADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIIKSLYATGFDDVRVETAD 80	
Db	21 ADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIIKSLYATGFDDVRVETAD 80	
Qy	81 GQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSYFNQATLNOAVAGLKEEY 140	
Db	81 GQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSYFNQATLNOAVAGLKEEY 140	
Qy	141 LGRGKLNIOITPKVTKLARNRVDIITIDEGKSAKITDIEFEGNQVYSDRKLWRQMSLTE 200	
Db	141 LGRGKLNIOITPKVTKLARNRVDIITIDEGKSAKITDIEFEGNQVYSDRKLWRQMSLTE 200	
Qy	201 GGIWTLTRSNQFNEQKFAQDMKVDFYQNGVYDFRILDTDIQTNEDTKTKITITVH 260	
Db	201 GGIWTLTRSNQFNEQKFAQDMKVDFYQNGVYDFRILDTDIQTNEDTKTKITITVH 260	
Qy	261 EGGFRMGKVSIEGDTNEVPKAELEKLLTMKPGKYERQQTAVLGEIQNRMGSAGYAYS 320	
Db	261 EGGFRMGKVSIEGDTNEVPKAELEKLLTMKPGKYERQQTAVLGEIQNRMGSAGYAYS 320	
Qy	321 EISVQPLPNAETKTVDVFLHIEPGRKTYVNEIHITGNKTRDEVVRRELQMESAPYDTS 380	
Db	321 EISVQPLPNAETKTVDVFLHIEPGRKTYVNEIHITGNKTRDEVVRRELQMESAPYDTS 380	
Qy	381 KLQSKERVLLGYFDNVQPDVAVPLAGTDPKVDLNMSLTERSTGSLDLSAGVQDGTGLVM 440	
Db	381 KLQSKERVLLGYFDNVQPDVAVPLAGTDPKVDLNMSLTERSTGSLDLSAGVQDGTGLVM 440	
Qy	441 SAGVSQDNLFCTGKSAALRASRSKTTLNGSLSFPTDPTADGVSLGVDYVGKAFDPRKAS 500	
Db	441 SAGVSQDNLFCTGKSAALRASRSKTTLNGSLSFPTDPTADGVSLGVDYVGKAFDPRKAS 500	
Qy	501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHYADFIKKYKTDG 560	
Db	501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHYADFIKKYKTDG 560	
Qy	561 TDGSFKGLVYKGTVGWRNKTDSALWPTGRVLTGVNAEIALPGSKLOYYSATNQWTFPP 620	
Db	561 TDGSFKGLVYKGTVGWRNKTDSALWPTGRVLTGVNAEIALPGSKLOYYSATNQWTFPP 620	
Qy	621 LSKTFTLMLGGEVGIAGGYGRTKEIPFFENFYGGGLGSRVGYESGTLGPKVYDEYGEKIS 680	
Db	621 LSKTFTLMLGGEVGIAGGYGRTKEIPFFENFYGGGLGSRVGYESGTLGPKVYDEYGEKIS 680	
Qy	681 YGGNKKANVASLELLFPMPGAKADARTVRLSLFADAGSVWMDGKTYDDNSSSATGGRVQNIYG 740	
Db	681 YGGNKKANVASLELLFPMPGAKADARTVRLSLFADAGSVWMDGKTYDDNSSSATGGRVQNIYG 740	
Qy	741 AGNTHKSTFTNELRYSGAGVATWLSPLGPMKF 772	

Db	741 AGNTHKSTFTNELRYSGAGVATWLSPLGPMKF 772	
RESULT 9		
AAB84746		
ID	AAB84746 standard; protein; 797 AA.	
XX		
AC	AAB84746;	
XX		
DT	17-SEP-2001 (first entry)	
XX		
DE	Amino acid sequence of a Neisseria serogroup A protein.	
XX		
KW	Serogroup A protein; outer membrane protein; Neisserial infection;	
KW	vaccine.	
XX		
OS	Neisseria meningitidis.	
PH	Key	Location/Qualifiers
FT	Peptide	1..21
FT	Protein	/note= "signal peptide"
FT		22..797
FT		/note= "mature protein"
XX		
PN	WO200152885-A1.	
XX		
PD	26-JUL-2001.	
XX		
PF	17-JAN-2001; 2001WO-1B000166.	
XX		
PR	17-JAN-2000; 2000GB-00001067.	
XX		
PR	09-MAR-2000; 2000GB-00005699.	
XX		
PA	(CHIR-) CHIRON SPA.	
XX		
PI	Pizza M, Rappuoli R, Giuliani M;	
XX		
DR	WPI; 2001-451895/48.	
DR	N-PSDB; AAH421130.	
XX		
PT	Composition for treating or preventing infection to, detecting, or for	
PT	raising antibodies against Neisserial bacteria, comprises an N.	
PT	meningitidis serogroup B outer membrane preparation and an immunogenic	
PT	component.	
XX		
PS	Disclosure; Page 71-74; 83pp; English.	
XX		
CC	The present sequence represents a Neisseria serogroup A protein. The	
CC	protein is used to produce the compositions of the invention. The	
CC	specification describes a composition, comprising a Neisseria	
CC	meningitidis serogroup B outer membrane preparation and an immunogenic	
CC	component. The immunogenic component is protein disclosed in WO99/57280,	
CC	WO99/36544, WO99/24578, WO99/66791, WO97/28273, WO96/29412, WO95/03413,	
CC	WO99/31132, WO99/58683, WO99/55873, and/or N. meningitidis protein PorA,	
CC	Tbpa, TbpB, PilC, Opa, or Omp85. The composition is used for making a	
CC	medicament for treating or preventing infection due to Neisserial	
CC	bacteria; a diagnostic reagent for detecting the presence of Neisserial	
CC	bacteria or of antibodies raised against Neisserial bacteria; and/or a	
CC	reagent which can raise antibodies against Neisserial bacteria. It may	
CC	also be used as a vaccine	
XX		
SQ	Sequence 797 AA;	
	Query Match 94.4%; Score 752; DB 4; Length 797;	
	Best Local Similarity 100.0%; Pred. No. 0;	
	Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	21 ADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIIKSLYATGFDDVRVETAD 80	
Db	21 ADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIIKSLYATGFDDVRVETAD 80	
Qy	81 GQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSYFNQATLNOAVAGLKEEY 140	



Db	81	QQLLTWIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSOYFNQATLNQAVAGLKEEY	140
Qy	141	LGRGKLNITQITPKVTKLARNRVDIDITIDEGSKAKITDIEFEGNQVYSDRKLARQMSLTE	200
Db	141	LGRGKLNITQITPKVTKLARNRVDIDITIDEGSKAKITDIEFEGNQVYSDRKLARQMSLTE	200
Qy	201	GGIWTWLTNRNQFNEQKFAQDMKVDFYQNNGVDFRILDTDIQTNEDEKTKQIKITVH	260
Db	201	GGIWTWLTNRNQFNEQKFAQDMKVDFYQNNGVDFRILDTDIQTNEDEKTKQIKITVH	260
Qy	261	EGGRFRMGKVSIEGDTNEVPKAELEKLLTMKPGKWERQQMTAVLGEIQNRMSGAGYAYS	320
Db	261	EGGRFRMGKVSIEGDTNEVPKAELEKLLTMKPGKWERQQMTAVLGEIQNRMSGAGYAYS	320
Qy	321	EISVQPLPNAETKTVDVFLHIIEPGRKIYVNEIHITGNKTRDEVRRELQMESAPYDTS	380
Db	321	EISVQPLPNAETKTVDVFLHIIEPGRKIYVNEIHITGNKTRDEVRRELQMESAPYDTS	380
Qy	381	KLQSKERVLLGYFDNVQFPAVLACTPPDKVDLNMSLTERSTGSLDLSAGWQDVTGLVM	440
Db	381	KLQSKERVLLGYFDNVQFPAVLACTPPDKVDLNMSLTERSTGSLDLSAGWQDVTGLVM	440
Qy	441	SAGVSQDNLFGTGSAALRASRSKTTLNGSLSFDPYFTADGVSIGYDVYKAFDPRKAS	500
Db	441	SAGVSQDNLFGTGSAALRASRSKTTLNGSLSFDPYFTADGVSIGYDVYKAFDPRKAS	500
Qy	501	TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHVADFIKKYKTDG	560
Db	501	TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHVADFIKKYKTDG	560
Qy	561	TGGSFKGHLVYGTGVGGRNKDTSALWPTRGYLTGVNAEIALPGSKLOVYSATHNQWFFP	620
Db	561	TGGSFKGHLVYGTGVGGRNKDTSALWPTRGYLTGVNAEIALPGSKLOVYSATHNQWFFP	620
Qy	621	LSKTFPLMGEGVGTAGVGRKTEIPFPENFYGGGLGVRGVESGTLGPKVYDEYGEKIS	680
Db	621	LSKTFPLMGEGVGTAGVGRKTEIPFPENFYGGGLGVRGVESGTLGPKVYDEYGEKIS	680
Qy	681	YGGNKKANVSARELLPMPGAKDARTVRLSLFADAGSVWDGKTYDDNSSATGGRVQNIYG	740
Db	681	YGGNKKANVSARELLPMPGAKDARTVRLSLFADAGSVWDGKTYDDNSSATGGRVQNIYG	740
Qy	741	AGNTHKSTFTNELRYSAGAVTWLSPLGPMKF	772
Db	741	AGNTHKSTFTNELRYSAGAVTWLSPLGPMKF	772
RESULT 10			
ID	AAB84744 standard; protein; 797 AA.		
XX			
AC	AAB84744;		
XX			
DT	17-SEP-2001 (first entry)		
XX			
DE	Amino acid sequence of a Neisseria serogroup B protein.		
XX			
KW	Serogroup B protein; outer membrane protein; Neisserial infection;		
KW	vaccine.		
XX	Neisseria meningitidis.		
XX			
FT	Key	Location/Qualifiers	
FT	Peptide	1..21	
FT		/note= "signal peptide"	
FT	Protein	22..797	
FT		/note= "mature protein"	
XX	WO200152885-A1.		
PN			
XX			
PD	26-JUL-2001.		
XX			
PF	17-JAN-2001; 2001WO-IB000166.		

XX	PR	17-JAN-2000; 2000GB-00001067.	
PR	09-MAR-2000; 2000GB-00005699.		
XX			
PA	(CHIR-) CHIRON SPA.		
XX			
PI	Pizza M, Rappuoli R, Giuliani M;		
XX			
DR	WPI; 2001-451895/48.		
DR	N-PSDB; AAH42128.		
XX			
XX	Composition for treating or preventing infection to, detecting, or for raising antibodies against Neisserial bacteria, comprises an N. meningitidis serogroup B outer membrane preparation and an immunogenic component.		
XX			
PS	Disclosure; Page 59-61; 83pp; English.		
XX			
CC	The present sequence represents a Neisseria serogroup B protein. The protein is used to produce the compositions of the invention. The specification describes a composition, comprising a Neisseria meningitidis serogroup B outer membrane preparation and an immunogenic component. The immunogenic component is protein disclosed in WO99/57280, WO99/36544, WO99/24578, WO99/66791, WO97/28273, WO96/29412, WO95/03413, WO99/31132, WO99/58683, WO99/55873, and/or N. meningitidis protein PorA, TbpA, TbpB, PilC, Opa, or Omp85. The composition is used for making a medicament for treating or preventing infection due to Neisserial bacteria; a diagnostic reagent for detecting the presence of Neisserial bacteria or of antibodies raised against Neisserial bacteria; and/or a reagent which can raise antibodies against Neisserial bacteria. It may also be used as a vaccine		
XX			
SQ	Sequence 797 AA;		
Query Match 94.4%; Score 752; DB 4; Length 797;			
Best Local Similarity 100.0%; Pred. No. 0;			
Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	21	ADFTIQDIRVEGQRTPESTVFNYPVKVGDYNDTHGSAIIKSLYATGTFDDVRVETAD	80
Db	21	ADFTIQDIRVEGQRTPESTVFNYPVKVGDYNDTHGSAIIKSLYATGTFDDVRVETAD	80
Qy	81	GQLLTWIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSOYFNQATLNQAVAGLKEEY	140
Db	81	GQLLTWIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSOYFNQATLNQAVAGLKEEY	140
Qy	141	LGRGKLNITQITPKVTKLARNRVDIDITIDEGSKAKITDIEFEGNQVYSDRKLARQMSLTE	200
Db	141	LGRGKLNITQITPKVTKLARNRVDIDITIDEGSKAKITDIEFEGNQVYSDRKLARQMSLTE	200
Qy	201	GGIWTWLTNRNQFNEQKFAQDMKVDFYQNNGVDFRILDTDIQTNEDEKTKQIKITVH	260
Db	201	GGIWTWLTNRNQFNEQKFAQDMKVDFYQNNGVDFRILDTDIQTNEDEKTKQIKITVH	260
Qy	261	EGGRFRMGKVSIEGDTNEVPKAELEKLLTMKPGKWERQQMTAVLGEIQNRMSGAGYAYS	320
Db	261	EGGRFRMGKVSIEGDTNEVPKAELEKLLTMKPGKWERQQMTAVLGEIQNRMSGAGYAYS	320
Qy	321	EISVQPLPNAETKTVDVFLHIIEPGRKIYVNEIHITGNKTRDEVRRELQMESAPYDTS	380
Db	321	EISVQPLPNAETKTVDVFLHIIEPGRKIYVNEIHITGNKTRDEVRRELQMESAPYDTS	380
Qy	381	KLQSKERVLLGYFDNVQFPAVLACTPPDKVDLNMSLTERSTGSLDLSAGWQDVTGLVM	440
Db	381	KLQSKERVLLGYFDNVQFPAVLACTPPDKVDLNMSLTERSTGSLDLSAGWQDVTGLVM	440
Qy	441	SAGVSQDNLFGTGSAALRASRSKTTLNGSLSFDPYFTADGVSIGYDVYKAFDPRKAS	500
Db	441	SAGVSQDNLFGTGSAALRASRSKTTLNGSLSFDPYFTADGVSIGYDVYKAFDPRKAS	500
Qy	501	TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHVADFIKKYKTDG	560
Db	501	TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHVADFIKKYKTDG	560

QY 561 TDGSPKGLYKGTGVGRNKTDSALWPTRGYLTVGNVNAEIALPGSKLOYYSATHNQWFFP 620  
Db 561 TDGSPKGLYKGTGVGRNKTDSALWPTRGYLTVGNVNAEIALPGSKLOYYSATHNQWFFP 620  
QY 621 LSKTFTMLGGEVGIAGGYGRTEIPFENFYGGGLGSRVGYESGTLGPKVYDEYGEKIS 680  
Db 621 LSKTFTMLGGEVGIAGGYGRTEIPFENFYGGGLGSRVGYESGTLGPKVYDEYGEKIS 680  
QY 681 YGNNKKNVSAELLFPMGAKDARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIYG 740  
Db 681 YGNNKKNVSAELLFPMGAKDARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIYG 740  
QY 741 AGNTHKSTFTNELRYSAGGAVTWLSPLGPMKF 772  
Db 741 AGNTHKSTFTNELRYSAGGAVTWLSPLGPMKF 772

RESULT 11  
AEB93431  
ID AEB93431 standard; protein; 797 AA.  
AC AEB93431;  
DT 20-OCT-2005 (first entry)  
XX Neisseria meningitidis group B outer membrane protein Omp85.  
DE protein quantitation; outer membrane protein Omp85.  
KW Neisseria meningitidis serogroup B.  
OS US2005176085-A1.  
PN 11-AUG-2005.  
XX 15-NOV-2004; 2004US-009888943.  
XX 19-NOV-2003; 2003CU-00000269.  
PR (BETA/) BETANCOURT N L H.  
PA (DORTA/) DORTA-DUQUE J F D C.  
PA (PERE/) PEREZ V A B.  
PA (VALD/) VALDES J G.  
PA (LOPE/) LOPEZ L J G.  
PA (PALO/) PALOMARES G R P.  
PA (FEYT/) FEYT R P.  
PA (GILF/) GIL F M A.

XX Betancourt NLH, Dorta-Duque JFD, Perez VAB, Valdes JG, Lopez LJG;  
PI Palomares GRP, Feyt RP, Gil FMA;  
XX WPI; 2005-596348/61.  
XX  
XX Identifying and quantifying proteins in complex mixtures by selectively  
PT isolating peptides not containing histidine nor arginine from each  
PT protein, and determining the relative concentration of proteins in  
PT different samples.  
XX  
XX Example 2; SEQ ID NO 7; 91pp; English.  
XX  
XX The invention relates to a method for identifying and quantifying one or  
CC more proteins in complex mixtures by selectively isolating peptides not  
CC containing histidine nor arginine (NHR peptides) from each protein, and  
CC determining the relative concentration of one or more proteins in  
CC different samples from the ratio between the areas of estimated  
CC theoretical spectra for each NHR peptide labeled with different isotopes  
CC in each sample. The method comprises: (a) enzymatically or chemically  
CC hydrolyzing the sample or samples of proteins; (b) chemically modifying  
CC alpha and epsilon amino groups (alpha- and epsilon-NH2) of every peptide  
CC obtained in step (a); (c) isolating the NHR peptides by cation exchange  
CC chromatography from the mixture of peptides obtained in step (b); (d)  
CC identifying proteins by mass spectrometry analysis of the NHR peptides

CC obtained in step (c); (e) differential isotopic labeling of protein  
CC samples previously to step (a) or during steps (a) or (b) and immediately  
CC mixing at least a portion of the samples; and (f) relative quantifying of  
CC more proteins in the mixtures of step (e) from the ratio between the  
CC areas of estimated theoretical spectra of the pair of NHR peptides  
CC identified in step (d), as well as from the ratio between the areas of  
CC the estimated theoretical spectra of fragments from the NHR peptides,  
CC generated in step (d). Also described is a kit for the identification and  
CC quantification of proteins in complex mixtures, which comprises the  
CC method mentioned above. The method and kit are useful for identifying or  
CC quantifying proteins, such as those with vaccinal, therapeutic or  
CC diagnostic uses, in complex mixtures. The present sequence represents an  
CC outer membrane protein Omp85, which is used in an example from the  
CC present invention.  
XX  
XX  
SQ Sequence 797 AA;  
Query Match 94.4%; Score 752; DB 9; Length 797;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 21 ADFTIQDIRVEGLQRTPESTVFNYPVKVGDYVNDTHGSAIIKSLYATGFFDDVRVETAD 80  
Db 21 ADFTIQDIRVEGLQRTPESTVFNYPVKVGDYVNDTHGSAIIKSLYATGFFDDVRVETAD 80  
QY 81 GQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSOYFNQATLNOAVAGLKEEY 140  
Db 81 GQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSOYFNQATLNOAVAGLKEEY 140  
QY 141 LGRGKLNIIQITPKVTKLARNRVDIDITIDEGKSAKITDIEFEGNQVYSDRKLQRMSLTE 200  
Db 141 LGRGKLNIIQITPKVTKLARNRVDIDITIDEGKSAKITDIEFEGNQVYSDRKLQRMSLTE 200  
QY 201 GGIWTLWTRSNQFNEQKFAQDMKVTDFYQNNGYDFRILDTDIQNEBKTKQTIKITH 260  
Db 201 GGIWTLWTRSNQFNEQKFAQDMKVTDFYQNNGYDFRILDTDIQNEBKTKQTIKITH 260  
QY 261 EGGFRFWGKVSIEGDTNEVPKAELEKLTWKPKWYEROQMTAVLGEIQNRMGSAVAYS 320  
Db 261 EGGFRFWGKVSIEGDTNEVPKAELEKLTWKPKWYEROQMTAVLGEIQNRMGSAVAYS 320  
QY 321 EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHIITGNKTRDEVVRRELQMESAPYDTS 380  
Db 321 EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHIITGNKTRDEVVRRELQMESAPYDTS 380  
QY 381 KLQRSKERVVELLYGFDNVQFADVPLAGTDPKVDLNNLSLTERSTGSLDLSAGWVQDTGLVM 440  
Db 381 KLQRSKERVVELLYGFDNVQFADVPLAGTDPKVDLNNLSLTERSTGSLDLSAGWVQDTGLVM 440  
QY 441 SAGVSDNLFGTCKSAALRASRSTKTLNGSLSFDPYFTADGVSLGVDYVYGKAFDPRKAS 500  
Db 441 SAGVSDNLFGTCKSAALRASRSTKTLNGSLSFDPYFTADGVSLGVDYVYGKAFDPRKAS 500  
QY 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHYADFIKKYKTDG 560  
Db 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHYADFIKKYKTDG 560  
QY 561 TDGSPKGLYKGTGVGRNKTDSALWPTRGYLTVGNVNAEIALPGSKLOYYSATHNQWFFP 620  
Db 561 TDGSPKGLYKGTGVGRNKTDSALWPTRGYLTVGNVNAEIALPGSKLOYYSATHNQWFFP 620  
QY 621 LSKTFTMLGGEVGIAGGYGRTEIPFENFYGGGLGSRVGYESGTLGPKVYDEYGEKIS 680  
Db 621 LSKTFTMLGGEVGIAGGYGRTEIPFENFYGGGLGSRVGYESGTLGPKVYDEYGEKIS 680  
QY 681 YGNNKKNVSAELLFPMGAKDARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIYG 740  
Db 681 YGNNKKNVSAELLFPMGAKDARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIYG 740  
QY 741 AGNTHKSTFTNELRYSAGGAVTWLSPLGPMKF 772  
Db 741 AGNTHKSTFTNELRYSAGGAVTWLSPLGPMKF 772



Db 121 SQYFNQATLNQAVAGKEEYVLGRGLNIQTTPKVTKLARNRVLDITIDEGRSKAITDIE 180  
 Qy 181 FEGNQVYSRDKLMRQMSLTGGGIWTWLTRS 210  
 |||||  
 Db 181 FEGNQVYSRDKLMRQMSLTGGGIWTWLTRS 210  
 |||||  
 RESULT 13  
 AAB23786  
 ID AAB23786 standard; protein; 792 AA.  
 XX AC AAB23786;  
 XX AC  
 XX 11-SEP-2003 (revised)  
 DT DT  
 DT 12-JAN-2001 (first entry)  
 XX  
 XX Neisseria gonorrhoeae amino acid sequence.  
 DE  
 XX CG motif; complete Freund's adjuvant; phosphorothioate; immunogenic;  
 KW Neisseria antigen; Neisseria meningitidis; Neisseria gonorrhoeae;  
 KW bactericidal; antibacterial; vaccine; immunostimulatory; infection;  
 KW immune response.  
 KW  
 XX Neisseria gonorrhoeae.  
 OS  
 XX WO200050075-A2.  
 PN  
 XX  
 XX 31-AUG-2000.  
 PD  
 XX  
 XX 09-FEB-2000; 2000WO-IB000176.  
 PF  
 XX  
 XX 26-FEB-1999; 99US-0121792P.  
 PR  
 XX  
 XX (CHIR-) CHIRON SPA.  
 PA  
 XX  
 XX Grandi G, Rappuoli R, Giuliani MM, Pizza M;  
 PI  
 XX WPI; 2001-015529/02.  
 DR  
 XX  
 XX Immunogenic composition useful for stimulating an immune response in a  
 PT mammal against Neisseria infection, comprises Neisseria antigen and an  
 PT adjuvant composition comprising an oligonucleotide with a CG motif.  
 XX  
 XX Claim 22; Page 32; 39pp; English.  
 PS  
 XX The present invention describes an immunogenic composition (I) comprising  
 CC a Neisseria antigen and an adjuvant composition comprising an  
 CC oligonucleotide comprising at least 1 CG motif. Also described is an  
 CC adjuvant composition (II) comprising an oligonucleotide which comprises  
 CC at least 1 CG motif and a complete Freund's adjuvant (CFA), where the  
 CC oligonucleotide preferably comprises at least one phosphorothioate bond.  
 CC AAA92359 to AAA92385 represent specifically claimed oligonucleotides of  
 CC the present invention. (I) is useful for stimulating an immune response  
 CC in a mammal, preferably a human, against Neisseria infection, preferably  
 CC Neisseria meningitidis infection and in the manufacture of a medicament  
 CC for inducing a protective immune response in a mammal. The present  
 CC sequence represents the claimed Neisseria gonorrhoeae amino acid sequence  
 CC disclosed in GB-9928197.4, which is given in the present invention.  
 CC (Updated on 11-SEP-2003 to standardise OS field)  
 XX  
 XX Sequence 792 AA;  
 SQ  
 Query Match 26.3%; Score 210; DB 4; Length 792;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-201;  
 Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0  
 Qy 1 MKLQIASALMMGLGISPLAFADFTIQDIRVSGLQRTPESTVFNPLPVKVGDTYNDTHGSA 60  
 Db 1 MKLQIASALMMGLGISPLAFADFTIQDIRVSGLQRTPESTVFNPLPVKVGDTYNDTHGSA 60  
 Qy 61 IIKSLIYATGFFDDVRVETADGQLLITVIERPTIGSLNITGAKMLQNDAIKKNLSEFGLAQ 120  
 |||||

RESULT 12  
AAU03958  
ID AAU03958 standard; protein; 792 AA.  
XX AC  
XX AAU03958;  
XX  
XX 23-OCT-2001 (first entry)  
XX  
XX Neisseria meningitidis serogroup A antigenic protein #1.  
DE Serogroup B antigen; pharynx; meningitis; septicaemia; mammalian cell;  
XX bacterial infection; baculovirus; yeast.  
KW  
XX Neisseria meningitidis.  
OS  
XX  
XX  
XX Key Location/Qualifiers  
FH Peptide 1. .21  
FT FT /note= "Signal peptide"  
FT Protein 22. .792  
FT FT /note= "Mature N. meningitidis serogroup A antigen"  
XX  
XX WO200138350-A2.  
XX  
XX 31-MAY-2001.  
XX  
XX 28-NOV-2000; 2000WO-IB001851.  
XX  
XX 29-NOV-1999; 99GB-00028197.  
XX 09-MAR-2000; 2000GB-00005698.  
XX  
XX (CHIR-) CHIRON SPA.  
XX (STAT-) STATENS INST FOLKEHELSE.  
XX  
XX Giuliani MM, Pizza M, Rappuoli R, Holst J;  
XX WPI; 2001-381285/40.  
XX N-PSDB; AAS07278.  
XX  
XX Novel 85 kDa antigen from Neisseria meningitidis and Neisseria  
FT gonorrhoeae, useful in the manufacture of a medicament for treating and  
PT preventing Neisserial bacteria infection.  
XX  
XX Claim 1; Page 66-68; 92pp; English.  
XX  
XX The sequence represents a Neisseria meningitidis serogroup A 85 kDa  
CC antigenic protein. Neisseria meningitidis colonises the pharynx, causing  
CC meningitis and, occasionally, septicaemia in the absence of meningitis.  
CC This antigenic protein is useful in the manufacture of a medicament for  
CC treating or preventing infection due to Neisseria bacteria, such as  
CC meningitis and septicaemia. It is also useful as a diagnostic reagent for  
CC detecting the presence of Neisseria bacteria or antibodies raised against  
CC Neisseria, and as a reagent for raising the antibodies. The Neisserial  
CC nucleotide sequences can be expressed in a variety of different  
CC expression systems, for example, mammalian cells, baculoviruses, plants,  
CC bacteria and yeast. Note: There are two versions of this sequence  
CC displayed in the specification (see AAU04451)  
XX  
XX Sequence 792 AA;  
XX  
XX Query Match 26.3%; Score 210; DB 4; Length 792;  
XX Best Local Similarity 100.0%; Pred. No. 3.8e-201;  
XX Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX 1 MKLQIASALMMIGISPLAFADFTIQDIRVEGQRTPEPTVFNLYPKVGDYNDTHGSA 60  
XX 1 MKLQIASALMMIGISPLAFADFTIQDIRVEGQRTPEPTVFNLYPKVGDYNDTHGSA 60  
XX  
XX 61 IIKSLYATGFFDDVRVETADGQLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120  
XX 61 IIKSLYATGFFDDVRVETADGQLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120  
XX  
XX 121 SQYFNQATLNOQAVAGLKEEYLGRGKLNITQITPKVTKLARNRVDIDITIDEGSAKITDIE 180

Db 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDIAIKKNLESFGLAQ 120

Qy 121 SOYFNQATLNQAVAGLKEEYLGROKLNIOITPKVTKLARNRVDIDITIDSGKSAKITDIE 180

Db 121 SOYFNQATLNQAVAGLKEEYLGROKLNIOITPKVTKLARNRVDIDITIDSGKSAKITDIE 180

Qy 181 FEGNQVYSDRKLQRQMSLTGEGGIWTLTRS 210

Db 181 FEGNQVYSDRKLQRQMSLTGEGGIWTLTRS 210

RESULT 14

AAB84745

ID AAB84745 standard; protein; 792 AA.

XX AC AAB84745;

XX XX

DT 11-SEP-2003 (revised)

DT 17-SEP-2001 (first entry)

XX Amino acid sequence of a Neisseria gonorrhoeae protein.

DE Serogroup B protein; outer membrane protein; Neisserial infection;

XX vaccine.

XX Neisseria gonorrhoeae.

OS

XX Key Location/Qualifiers

FH Peptide 1..21

FT /notes="signal peptide"

FT Protein 22..792

FT /notes="mature protein"

XX WO200152885-A1.

XX XX

XX 26-JUL-2001.

XX

PF 17-JAN-2001; 2001WO-IB000166.

XX

XX 17-JAN-2000; 2000GB-00001067.

PR 09-MAR-2000; 2000GB-00005699.

XX

XX (CHIR-) CHIRON SPA.

PA

XX Pizza M, Rappuoli R, Giuliani M;

PI

XX WPI; 2001-451895/48.

DR N-PSDB; AAH42129.

DR

XX Composition for treating or preventing infection to, detecting, or for

PT raising antibodies against Neisserial bacteria, comprises an N.

PT meningitidis serogroup B outer membrane preparation and an immunogenic

PT component.

XX

XX Disclosure; Page 65-67; 83pp; English.

PS

XX The present sequence represents a Neisseria gonorrhoeae protein. The

CC protein is used to produce the compositions of the invention. The

CC specification describes a composition, comprising a Neisseria

CC meningitidis serogroup B outer membrane preparation and an immunogenic

CC component. The immunogenic component is protein disclosed in WO99/57280,

CC WO99/36544, WO99/24578, WO99/66791, WO97/28273, WO96/29412, WO95/03413,

CC WO99/31132, WO99/58683, WO99/55873, and/or N. meningitidis protein PorA,

CC TbpA, TbpB, PilC, Opa, or Omp85. The composition is used for making a

CC medicament for treating or preventing infection due to Neisserial

CC bacteria; a diagnostic reagent for detecting the presence of Neisserial

CC bacteria or of antibodies raised against Neisserial bacteria; and/or a

CC reagent which can raise antibodies against Neisserial bacteria. It may

CC also be used as a vaccine. (Updated on 11-SEP-2003 to standardise OS

CC field)

XX

XX Sequence 792 AA;

Qy

Query Match 26.3%; Score 210; DB 4; Length 792;

Best Local Similarity 100.0%; Pred. No. 3.8e-201; Indels 0; Gaps 0;

Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60

Db 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60

Qy 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDIAIKKNLESFGLAQ 120

Db 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDIAIKKNLESFGLAQ 120

Qy 121 SOYFNQATLNQAVAGLKEEYLGROKLNIOITPKVTKLARNRVDIDITIDSGKSAKITDIE 180

Db 121 SOYFNQATLNQAVAGLKEEYLGROKLNIOITPKVTKLARNRVDIDITIDSGKSAKITDIE 180

Qy 181 FEGNQVYSDRKLQRQMSLTGEGGIWTLTRS 210

Db 181 FEGNQVYSDRKLQRQMSLTGEGGIWTLTRS 210

RESULT 15

ABP80499

ID ABP80499 standard; protein; 792 AA.

XX AC ABP80499;

XX XX

DT 07-MAR-2003 (first entry)

DE N. gonorrhoeae amino acid sequence SEQ ID 7538.

XX Antibacterial; infection; vaccine; gene therapy.

XX Neisseria gonorrhoeae.

OS

XX WO200279243-A2.

PN

XX 10-OCT-2002.

PD

XX

XX 12-FEB-2002; 2002WO-IB002069.

PF

XX 12-FEB-2001; 2001GB-00003424.

PR

XX (CHIR-) CHIRON SPA.

PA

XX Fontana MR, Pizza M, Masignani V, Monaci E;

PI

XX WPI; 2003-058415/05.

DR N-PSDB; ABZ41469.

DR

XX New protein from Neisseria gonorrhoeae, useful for the manufacture of a

PT medicament for treating or preventing N. gonorrhoeae infection.

PT

XX Disclosure; Page 736; 815pp; English.

PS

XX The present invention relates to proteins from Neisseria gonorrhoeae.

CC Also disclosed are the nucleic acid molecules encoding the proteins and

CC antibodies that specifically bind to the proteins. The composition

CC comprising the protein, nucleic acid or antibody is useful for the

CC manufacture of a medicament for treating or preventing N. gonorrhoeae

CC infection, this may be in the form of a vaccine or gene therapy.

CC Sequences given in records ABP76736-ABP81046 represent nucleic acid

CC molecules of the invention

XX

XX Sequence 792 AA;

Qy

Query Match 26.3%; Score 210; DB 6; Length 792;

Best Local Similarity 100.0%; Pred. No. 3.8e-201; Indels 0; Gaps 0;

Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60

Db 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60

Qy	61	IIKS	YATG	FFDD	VRVET	ADGOLL	TTVIER	PTIG	SLNIT	GAKML	QND	AIKKN	LES	FGLAQ	120
Db	61	IIKS	YATG	FFDD	VRVET	ADGOLL	TTVIER	PTIG	SLNIT	GAKML	QND	AIKKN	LES	FGLAQ	120
Qy	121	SOYF	NOAT	LNQ	AVAG	LKEE	YLG	RKLN	IQIT	PKVT	KLARN	RVD	IDIT	IDE	KS
															180
Db	121	SOYF	NOAT	LNQ	AVAG	LKEE	YLG	RKLN	IQIT	PKVT	KLARN	RVD	IDIT	IDE	KS
															180
Qy	181	FE	GNQV	SDR	KLM	RQMS	LT	EGGI	WT	LT	RS	210			
Db	181	FE	GNQV	SDR	KLM	RQMS	LT	EGGI	WT	LT	RS	210			

Search completed: April 12, 2006, 16:19:10  
Job time : 231 secs

**This Page Blank (uspto)**

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 12, 2006, 16:15:32 ; Search time 235 Seconds

(without alignments)  
2392.792 Million cell updates/sec

Title: US-10-606-618-4

Perfect score: 797

Sequence: 1 MKLKQIASALMMLGISPLAF.....LKKPDEIQRFQQLGTTP 797

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : UniProt 05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	797	100.0	797	2	O30912_NEIME
2	752	94.4	797	2	O9JX31_NEIME
3	752	94.4	797	2	O9K1H0_NEIME
4	210	26.3	792	2	O5F5W8_NEIG1
5	157	19.7	792	2	P95359_NEIGO
6	13	1.6	771	2	Q7NVY6_CHRVO
7	13	1.6	786	2	Q8MH2_PSEPK
8	13	1.6	787	2	Q8H14_PSEPK
9	10	1.3	765	2	Q8XZ13_RALSO
10	10	1.3	766	2	Q5NZG7_AZOSE
11	9	1.1	328	2	Q9SNM7_ARATH
12	9	1.1	361	2	Q6L543_ORYSA
13	9	1.1	362	2	Q5PP51_ARATH
14	9	1.1	435	2	Q9LXP7_ARATH
15	9	1.1	713	2	Q9ZAB1_THETH
16	9	1.1	713	2	Q5GJ75_THETH
17	9	1.1	713	2	Q72J38_THETH
18	9	1.1	769	2	Q4LNA0_9BURK
19	9	1.1	769	2	Q63T20_BURPS
20	9	1.1	769	2	Q62JD2_BURMA
21	9	1.1	778	2	Q7VVC2_BORPE
22	9	1.1	778	2	Q7WA52_BORPA
23	9	1.1	778	2	Q7WJ86_BORBR
24	9	1.1	796	2	Q4KHG8_PSEF5
25	9	1.1	797	2	Q9S341_PHOLU
26	9	1.1	797	2	Q7N8N9_PHOTO
27	9	1.1	952	2	Q8COX4_MOUSE
28	9	1.1	1035	2	Q9M7J0_POPUL
29	8	1.0	55	2	Q8MTZ8_HETGL
30	8	1.0	82	1	YIM3_BEPI1
31	8	1.0	129	2	Q97L79_CLOAB

32	8	1.0	168	2	Q51R59_MAGGR
33	8	1.0	186	2	Q9ATW3_ZEA
34	8	1.0	215	2	Q52K81_ARATH
35	8	1.0	225	2	Q6B441_LEMMI
36	8	1.0	225	2	Q9ZU33_ARATH
37	8	1.0	241	2	Q8H308_ORYSA
38	8	1.0	259	2	Q4J118_ICTFU
39	8	1.0	273	2	Q5E535_VIBF1
40	8	1.0	277	2	Q87PJ6_VIBPA
41	8	1.0	287	2	Q7XM73_ORYSA
42	8	1.0	290	2	Q6FRT4_CANGA
43	8	1.0	299	2	Q8NSK6_CORGL
44	8	1.0	321	2	Q86GZ0_RHIAP
45	8	1.0	333	1	GYAR_PYRO
46	8	1.0	334	1	GYAR_PYRHO
47	8	1.0	334	2	Q8MTY1_RHIAP
48	8	1.0	335	2	GYAR_PYPAB
49	8	1.0	337	2	Q9KRW5_VIBCH
50	8	1.0	341	2	Q9SE52_9FABA
51	8	1.0	356	2	Q60BQ6_METCA
52	8	1.0	396	2	Q565X4_9BACT
53	8	1.0	426	2	Q81885_ARATH
54	8	1.0	428	2	Q75JP2_DICDI
55	8	1.0	429	1	FLIK_BACSU
56	8	1.0	439	2	Q7XFL9_ORYSA
57	8	1.0	439	2	Q8S7B4_ORYSA
58	8	1.0	447	2	Q65ET9_BACLD
59	8	1.0	461	2	Q93ZN9_ARATH
60	8	1.0	474	2	Q9T200_BPPH1
61	8	1.0	529	2	Q67NE9_SYMTH
62	8	1.0	552	2	Q5BA86_EMENI
63	8	1.0	558	2	Q7XK07_ORYSA
64	8	1.0	558	2	Q7XM75_ORYSA
65	8	1.0	583	2	Q911V1_PSEAE
66	8	1.0	614	2	Q4WN21_ASPFU
67	8	1.0	709	2	Q5BK84_RAT
68	8	1.0	731	2	Q57U79_9TRYP
69	8	1.0	758	2	Q82U03_NITEU
70	8	1.0	796	2	Q604T9_METCA
71	8	1.0	825	2	Q6FCG7_ACIAD
72	8	1.0	826	2	Q8EGG7_SHEON
73	8	1.0	897	2	Q5AFB7_CANAL
74	8	1.0	903	1	MSPI1_SCHPO
75	8	1.0	948	2	Q500C2_PSESY
76	8	1.0	1024	2	Q4MUX2_BACCE
77	8	1.0	1025	2	Q4V1M8_BACC2
78	8	1.0	1035	2	Q57XC5_9TRYP
79	8	1.0	1066	2	Q6NP12_DROME
80	8	1.0	1085	2	Q8FQNO_COREF
81	8	1.0	1107	2	Q5BDB6_EMENI
82	8	1.0	1286	2	Q5ARD3_EMENI
83	8	1.0	1353	2	Q5AS15_EMENI
84	8	1.0	1363	1	ILPR_BRALA
85	8	1.0	1459	2	Q75G47_ORYSA
86	8	1.0	1475	2	Q9LOU6_ARATH
87	8	1.0	1548	2	Q4SU16_TETNG
88	8	1.0	1577	1	HLVA_PROMI
89	8	1.0	2408	2	Q9V549_DROME
90	8	1.0	2903	2	Q4GZ26_9TRYP
91	8	1.0	4919	2	Q9ZHL0_HAEDU
92	8	1.0	6199	2	Q6JANO_BRARE
93	7	0.9	37	2	Q4XRS3_PLACH
94	7	0.9	53	2	Q4X6P2_PLACH
95	7	0.9	62	2	Q4K8A2_PSEF5
96	7	0.9	63	2	Q8TE37_HUMAN
97	7	0.9	65	2	Q8ZUE9_NITEU
98	7	0.9	67	2	Q8TMO2_STRCL
99	7	0.9	71	2	Q8XM23_CLOPE
100	7	0.9	75	2	Q83LO3_SHIFL
101	7	0.9	76	2	Q8X5D6_ECO57
102	7	0.9	76	1	DICC_ECOLI
103	7	0.9	85	2	Q4NKU1_9MICC
104	7	0.9	85	2	Q6D0U7_ERWCT

Q51R59	magnaporthe
Q9ATW3	zea mays (m
Q52K81	arabidopsis
Q6B441	lemna minor
Q9ZU33	arabidopsis
Q8H308	oryza sativ
Q4J118	icalurus p
Q5E535	vibrio fisc
Q87PJ6	vibrio para
Q7XM73	oryza sativ
Q6FRT4	candida gla
Q8NSK6	corynebacte
Q86GZ0	rhinicephal
Q5JE22	pyrococcus
Q58320	pyrococcus
Q8MTY1	rhinicephal
Q9UYR1	pyrococcus
Q9KRW5	vibrio chol
Q9SE52	eriosema ps
Q60BQ6	methyllococc
Q565X4	uncultured
Q81885	arabidopsis
Q75JR2	dictyosteli
P23451	bacillus su
Q7XFL9	oryza sativ
Q8S7B4	oryza sativ
Q65ET9	bacillus li
Q93ZN9	arabidopsis
Q9T200	bacterioph
Q67NE9	symbiobacte
Q5BA86	aspergillus
Q7XK07	oryza sativ
Q7XM75	oryza sativ
Q911V1	pseudomonas
Q4WN21	aspergillus
Q5BK84	rattus norv
Q57U79	trypanosoma
Q82U03	nitrosomona
Q604T9	methyllococc
Q6FCG7	acinetobact
Q8EGG7	shewanella
Q5AFB7	candida alb
P87320	schizosacch
Q500C2	pseudomonas
Q4MUX2	bacillus ce
Q4V1M8	bacillus ce
Q57XC5	trypanosoma
Q6NP12	drosophila
Q8FQNO	corynebacte
Q5BDB6	aspergillus
Q5ARD3	aspergillus
Q5AS15	aspergillus
Q02466	branchiosco
Q75G47	oryza sativ
Q91QU6	arabidopsis
Q4SU16	tetraodon n
P16466	proteus mir
Q9V549	drosophila
Q4GZ26	trypanosoma
Q9ZHL0	haemophilus
Q6JANO	brachydanio
Q4XRS3	plasmodium
Q4X6P2	plasmodium
Q4K8A2	pseudomonas
Q8CE37	homo sapien
Q8ZUE9	nitrosomona
Q8TMO2	streptomyce
Q8XM23	clostridium
Q83LO3	shigella fl
Q8X5D6	escherichia
P06965	escherichia
Q4NKU1	arthrobacte
Q6D0U7	erwinia car

105	7	0.9	89	2	Q5GT88_WOLTR	Q5gte8 wolbachia s	178	7	0.9	170	2	Q5MQF9_BRAJA	Q5mqf9 bradyrhizob
106	7	0.9	92	2	Q4KA61_PSEFS	Q4ka61 pseudomonas	179	7	0.9	170	2	Q5MQF6_BRAJA	Q5mqf6 bradyrhizob
107	7	0.9	93	2	Q726R5_DESVH	Q726r5 desulfovibr	180	7	0.9	171	2	Q9ZAL7_LISIV	Q9zal7 listeria iv
108	7	0.9	95	2	Q9XXG0_CAEEL	Q9xxg0 caenorhabdi	181	7	0.9	171	2	Q97QH7_STRPN	Q97qh7 streptococ
109	7	0.9	98	2	Q6G599_BARHE	Q6g599 bartonella	182	7	0.9	172	2	Q9JGT9_9RHAB	Q9jgt9 northern ce
110	7	0.9	101	1	PHS_STRCO	Q86722 streptomyce	183	7	0.9	175	2	Q4WDX4_ASPFU	Q4wdx4 aspergillus
111	7	0.9	101	2	Q76445_CAEEL	Q76445 caenorhabdi	184	7	0.9	175	2	Q9SVE4_ARATH	Q9sve4 arabidopsis
112	7	0.9	102	1	RLZ1_METKA	Q8tuu3 methanopyru	185	7	0.9	176	2	Q8SRN5_ENCCU	Q8srn5 encephalito
113	7	0.9	104	2	Q9IN54_9VIRU	Q9in54 citrus psor	186	7	0.9	177	2	Q676Z8_9ASPA	Q676z8 hyacinthus
114	7	0.9	104	2	Q9IN56_9VIRU	Q9in56 citrus psor	187	7	0.9	177	2	Q9R8W8_9RHIZ	Q9r8w8 rhizobium s
115	7	0.9	104	2	Q9IN57_9VIRU	Q9in57 citrus psor	188	7	0.9	177	2	Q9R8X0_9RHIZ	Q9r8x0 rhizobium s
116	7	0.9	104	2	Q9IN58_9VIRU	Q9in58 citrus psor	189	7	0.9	177	2	Q9R8X1_9RHIZ	Q9r8x1 rhizobium s
117	7	0.9	104	2	Q9IN59_9VIRU	Q9in59 citrus psor	190	7	0.9	177	2	Q9R8X2_9RHIZ	Q9r8x2 rhizobium s
118	7	0.9	104	2	Q9IN60_9VIRU	Q9in60 citrus psor	191	7	0.9	177	2	Q9ZJN0_9RHIZ	Q9zjn0 rhizobium s
119	7	0.9	109	2	Q4SYU5_AERPE	Q9y9u5 aeropyrum p	192	7	0.9	177	2	Q5WF12_9BRAD	Q5wfp12 bradyrhizob
120	7	0.9	109	2	Q4SBE1_TETNG	Q4sbel tetraodon n	193	7	0.9	177	2	Q5WF10_9BRAD	Q5wfp10 bradyrhizob
121	7	0.9	113	2	Q5QU24_IDILO	Q5qu24 idiomarina	194	7	0.9	177	2	Q5WP09_9BRAD	Q5wp09 bradyrhizob
122	7	0.9	115	2	Q7S7S3_NEUCR	Q7s7s3 neurospora	195	7	0.9	177	2	Q5WP08_9BRAD	Q5wp08 bradyrhizob
123	7	0.9	115	2	Q8RSN6_BACT	Q8rsn6 uncultured	196	7	0.9	177	2	Q5WP07_9BRAD	Q5wp07 bradyrhizob
124	7	0.9	118	2	Q59TAL_CANAL	Q59tal candida alb	197	7	0.9	177	2	Q5WP06_9BRAD	Q5wp06 bradyrhizob
125	7	0.9	120	2	Q6COL2_KLUJA	Q6col2 kluyveromyc	198	7	0.9	178	2	Q9ZJN4_9RHIZ	Q9zjn4 rhizobium s
126	7	0.9	123	1	KNG_GADMO	P83856 gadus morhu	199	7	0.9	179	2	Q6H0X9_9CREN	Q6h0x9 sulfolobus
127	7	0.9	123	2	Q7QBVL_ANOGA	Q7qbvl anopheles g	200	7	0.9	180	2	Q84IV2_MYCLE	Q84iv2 mycobacteri
128	7	0.9	124	1	CRCB_PHOLL	Q7n768 photorhabdu	201	7	0.9	184	2	Q26429_METTH	Q26429 methanobact
129	7	0.9	125	2	Q4ZT38_PSESY	Q4zt38 pseudomonas	202	7	0.9	184	2	Q6NE26_VIRU	Q6ne26 leptospira
130	7	0.9	126	2	Q9VW79_DROME	Q9vw79 drosophila	203	7	0.9	184	2	Q6FCT9_ACTAD	Q6fct9 acinetobact
131	7	0.9	127	2	Q06096_METMP	Q06096 methanococ	204	7	0.9	185	2	Q63WA2_BURPS	Q63wa2 burkholderi
132	7	0.9	128	2	Q9C266_NEUCR	Q9c266 neurospora	205	7	0.9	185	2	Q62LF2_BURMA	Q62lf2 burkholderi
133	7	0.9	130	2	Q9PVL4_9PERC	Q9pvl4 mola mola (	206	7	0.9	187	2	Q83NG0_TROW8	Q83ng0 tropheryma
134	7	0.9	130	2	Q76CV7_CONMY	Q76cv7 conger myri	207	7	0.9	189	2	Q4RR79_TETNG	Q4rr79 tetraodon n
135	7	0.9	131	2	Q93773_3ARCH	Q93773 uncultured	208	7	0.9	190	2	Q782U6_9ALPH	Q782u6 gallid herp
136	7	0.9	131	2	Q9A7L3_CAUCR	Q9a7l3 caulobacter	209	7	0.9	190	2	Q9QTE3_9ALPH	Q9qte3 marea's dis
137	7	0.9	133	2	Q58LE7_9CAUD	Q58le7 cyanophage	210	7	0.9	193	2	Q8VUA8_9LACT	Q8vua8 lactococcus
138	7	0.9	133	2	Q5ENK0_HETTR	Q5enk0 heterocapsa	211	7	0.9	194	2	Q6CY36_KLUJA	Q6cy36 kluyveromyc
139	7	0.9	134	2	Q8PN27_XANAC	Q8pn27 xanthomonas	212	7	0.9	194	2	Q7XVA3_GRIJA	Q7xva3 griffithsia
140	7	0.9	135	2	Q45783_CAEEL	Q45783 caenorhabdi	213	7	0.9	196	2	Q8LMY9_ORYSA	Q8lmv9 oryza sativ
141	7	0.9	138	2	Q7X116_9BACT	Q7x116 leptospiril	214	7	0.9	196	2	Q7THD4_9PICO	Q7thd4 aichi virus
142	7	0.9	139	2	Q7RZL4_NEUCR	Q7rzl4 neurospora	215	7	0.9	196	2	Q7THD5_9PICO	Q7thd5 aichi virus
143	7	0.9	140	2	Q9EMS9_AMEPV	Q9em9 amsacta moo	216	7	0.9	196	2	Q7THD6_9PICO	Q7thd6 aichi virus
144	7	0.9	143	2	Q5GUV4_XANOR	Q5guv4 xanthomonas	217	7	0.9	197	2	Q4FPR2_9RICK	Q4fpr2 candidatus
145	7	0.9	143	2	Q5KW12_GEOKA	Q5kw12 geobacillus	218	7	0.9	197	2	Q83N11_TROWT	Q83n11 tropheryma
146	7	0.9	145	2	Q91110_WORSA	Q91110 worone saxa	219	7	0.9	199	2	Q62M56_BURMA	Q62m56 burkholderi
147	7	0.9	148	2	Q50574_BACPF	Q50574 bacillus ps	220	7	0.9	202	1	HIS7_RHIME	Q92tb0 rhizobium m
148	7	0.9	150	1	SSRP_CAMJE	Q9pni9 campylobact	221	7	0.9	205	2	Q6CVD5_KLUJA	Q6cvd5 kluyveromyc
149	7	0.9	150	1	SSRP_CAMJE	Q5htn9 campylobact	222	7	0.9	207	1	THIE_CHRVO	Q7p1r3 chromobacte
150	7	0.9	150	2	Q4HGP9_CAMCO	Q4hgp9 campylobact	223	7	0.9	207	2	Q7PXH3_ANOGA	Q7pxh3 anopheles g
151	7	0.9	150	2	Q6DSB1_ERWCT	Q6dsb1 erwinia car	224	7	0.9	210	2	Q5WID5_BACSG	Q5wid5 bacillus cl
152	7	0.9	151	2	Q5LA18_BACFN	Q5la18 bacteroides	225	7	0.9	212	2	Q5EJ95_LACAC	Q5ej95 lactobacill
153	7	0.9	154	2	Q4HEM1_9DEIO	Q4hml deinococcus	226	7	0.9	214	1	NODB_RHIGA	Q503s4 rhizobium g
154	7	0.9	156	2	Q70T64_CIOIN	Q70t64 ciona intes	227	7	0.9	214	2	Q627B7_CABBR	Q627b7 caenorhabdi
155	7	0.9	157	2	Q8ETJ7_OCEIH	Q8etj7 oceanobacil	228	7	0.9	214	2	Q9CD65_MYCLE	Q9cd65 mycobacteri
156	7	0.9	163	2	Q8ETJ7_ARATH	Q8etj7 arabidopsis	229	7	0.9	216	2	Q6FXH5_CANGA	Q6fxh5 candida gla
157	7	0.9	164	2	Q7R6G1_GIALA	Q7r6g1 giardia lam	230	7	0.9	216	2	Q7NFC9_GLOVI	Q7nfc9 gloeobacter
158	7	0.9	165	2	Q6EPF5_ORYSA	Q6epf5 oryza sativ	231	7	0.9	218	2	Q9Z5F9_MYCLE	Q9z5f9 mycobacteri
159	7	0.9	168	2	Q9DKM2_9VIRU	Q9dkm2 spodoptera	232	7	0.9	218	2	Q63YC9_BURPS	Q63yc9 burkholderi
160	7	0.9	169	1	YLZ6_CAEEL	P34419 caenorhabdi	233	7	0.9	218	2	Q62EU7_BURMA	Q62eu7 burkholderi
161	7	0.9	169	2	Q60YR5_CAEBR	Q60yr5 caenorhabdi	234	7	0.9	221	2	Q8KK26_PROVU	Q8kk26 proteus vul
162	7	0.9	170	2	Q5MQH4_9BRAD	Q5mqh4 bradyrhizob	235	7	0.9	221	2	Q6D4J2_ERWCT	Q6d4j2 erwinia car
163	7	0.9	170	2	Q5MQG6_9BRAD	Q5mqg6 bradyrhizob	236	7	0.9	223	1	KCY_NITEU	Q82t5 nitrosomona
164	7	0.9	170	2	Q5MQG0_9BRAD	Q5mqg0 bradyrhizob	237	7	0.9	223	2	Q4TNP6_9SPHN	Q4tnp6 erythrobact
165	7	0.9	170	2	Q5MQF3_9BRAD	Q5mqf3 bradyrhizob	238	7	0.9	225	2	Q8KT67_PHOJU	Q8kt67 photorhabdu
166	7	0.9	170	2	Q5MQF0_9BRAD	Q5mqf0 bradyrhizob	239	7	0.9	225	2	Q7N025_PHOUL	Q7n025 photorhabdu
167	7	0.9	170	2	Q5MQS7_9BRAD	Q5mqe7 bradyrhizob	240	7	0.9	226	2	Q9VLK7_DROME	Q9v1k7 drosophila
168	7	0.9	170	2	Q5MQS4_9BRAD	Q5mqe4 bradyrhizob	241	7	0.9	226	2	Q96SW3_CAEEL	Q96sw3 caenorhabdi
169	7	0.9	170	2	Q5MQS3_9BRAD	Q5mqe3 bradyrhizob	242	7	0.9	227	2	Q63S36_BURPS	Q63s36 burkholderi
170	7	0.9	170	2	Q5MQS2_9BRAD	Q5mqe2 bradyrhizob	243	7	0.9	227	2	Q5Q2P8_IDILO	Q5q2p8 idiomarina
171	7	0.9	170	2	Q5MQS0_9BRAD	Q5mqe0 bradyrhizob	244	7	0.9	228	2	Q9EMK6_AMEPV	Q9emk6 amsacta moo
172	7	0.9	170	2	Q5MQS8_9BRAD	Q5mqe8 bradyrhizob	245	7	0.9	230	2	Q7QBH1_ANOGA	Q7qbh1 anopheles g
173	7	0.9	170	2	Q5MQH2_9BRAD	Q5mqh2 bradyrhizob	246	7	0.9	231	2	Q4VMH3_9EURO	Q4vmh3 neosartoria
174	7	0.9	170	2	Q5MQD8_9BRAD	Q5mqd8 bradyrhizob	247	7	0.9	231	2	Q4VMH5_9EURO	Q4vmh5 neosartoria
175	7	0.9	170	2	Q5MQS5_BRAEL	Q5mqes bradyrhizob	248	7	0.9	231	2	Q53LL3_ORYSA	Q53ll3 oryza sativ
176	7	0.9	170	2	Q5MQG3_9BRAD	Q5mqg3 bradyrhizob	249	7	0.9	231	2	Q4K719_PSEFS	Q4k719 pseudomonas
177	7	0.9	170	2	Q5MQF1_BRAJA	Q5mqf1 bradyrhizob	250	7	0.9	231	2	Q5LWAB_SILPO	Q5lwa8 silicibacte

251	7	0.9	233	2	Q9RJPL_STRCO	Q9RJPL streptomyc
252	7	0.9	233	2	Q7U5M9_SYNXP	Q7U5m9 synchococc
253	7	0.9	234	2	Q25327_HELPJ	Q25327 hellicobacte
254	7	0.9	234	2	Q25327_HELPJ	Q25327 hellicobacte
255	7	0.9	235	2	Q7NWX8_CHRNO	Q7nwx8 chromabacte
256	7	0.9	238	2	Q7NWB10_WAGVO	Q7nwb10 pachysandra
257	7	0.9	238	2	Q4ZU73_PSESY	Q4zu73 pseudomonas
258	7	0.9	238	2	Q4ZU73_PSESY	Q4zu73 pseudomonas
259	7	0.9	238	2	Q82YK6_PSEAE	Q82y6 pseudomonas
260	7	0.9	241	2	Q68961_HELPY	Q68961 hellicobacte
261	7	0.9	242	2	Q5J161_PYRKO	Q5j161 pyrococcus
262	7	0.9	242	2	Q6GMW5_9NAGN	Q6gmw5 akedia trif
263	7	0.9	242	2	Q7U774_SYNXP	Q7u774 synchococc
264	7	0.9	243	2	Q7N9U3_PHOLL	Q7n9u3 photorhabdu
265	7	0.9	243	2	Q82YK6_PSEAE	Q82y6 pseudomonas
266	7	0.9	246	2	Q60110_MYCHA	Q60110 mycoplasma
267	7	0.9	246	2	Q98FG4_RHILO	Q98fg4 rhizobium 1
268	7	0.9	248	2	Q8PUT8_METMA	Q8put8 methanosarc
269	7	0.9	248	2	Q98K42_RHILO	Q98k42 rhizobium 1
270	7	0.9	249	2	Q8TJK1_METAC	Q8tjk1 methanosarc
271	7	0.9	249	2	Q8LAW6_BACCR	Q8law6 bacillus ce
272	7	0.9	254	2	Q7SAF5_NEUCR	Q7saf5 neurospora
273	7	0.9	254	2	Q946T1_SORBI	Q946t1 sorghum bic
274	7	0.9	255	2	Q8CY97_STRR6	Q8cy97 streptococc
275	7	0.9	255	2	Q97NR2_STRPN	Q97nr2 streptococc
276	7	0.9	255	2	Q5FRW9_GLUOX	Q5frw9 gluconobact
277	7	0.9	256	2	Q4K6W1_PSEF5	Q4k6w1 pseudomonas
278	7	0.9	257	1	HADD_RHISH	Q8K189 rhizobium s
279	7	0.9	259	2	Q5YTX5_NOCFA	Q5ytx5 nocardia fa
280	7	0.9	260	2	Q87ST1_VIBPA	Q87st1 vibrio para
281	7	0.9	264	2	Q4TLN6_GIBZE	Q4tlne gibberella
282	7	0.9	264	2	Q8NSS7_DROME	Q8nss7 drosophila
283	7	0.9	264	2	Q5L6W4_CHLAB	Q5l6w4 chlamydophi
284	7	0.9	264	2	Q84478_CHLTR	Q84478 chlamydia t
285	7	0.9	264	2	Q5YPD0_NOCFA	Q5ydp0 nocardia fa
286	7	0.9	264	2	Q824J5_CHLVC	Q824j5 chlamydophi
287	7	0.9	264	2	Q9P1S1_CHLMU	Q9p1s1 chlamydia m
288	7	0.9	265	2	Q4FUC8_9GNMM	Q4fuc8 psychrobact
289	7	0.9	266	2	Q5LSY3_CHLAB	Q5lsy3 chlamydophi
290	7	0.9	266	2	Q8CES7_MOUSE	Q8ces7 mus musculu
291	7	0.9	267	2	Q6I173_DROME	Q6i173 drosophila
292	7	0.9	267	2	Q893R1_CLOTE	Q893r1 clostridium
293	7	0.9	267	2	Q7AC45_GEOSL	Q7ac45 geobacter s
294	7	0.9	267	2	Q7NGC2_GLOVI	Q7ngc2 gloeobacter
295	7	0.9	268	1	AROK_THEAC	Q9nle5 thermoplasma
296	7	0.9	268	2	Q86780_STRCO	Q86780 streptomyc
297	7	0.9	269	2	Q81IU2_PLAF7	Q81iu2 plasmodium
298	7	0.9	269	2	Q9XAC7_STRCO	Q9xac7 streptomyc
299	7	0.9	270	2	Q6BT18_DEBHA	Q6bri8 debaryomyc
300	7	0.9	272	2	Q5L112_BACFN	Q5l112 bacteroides
301	7	0.9	272	2	Q64ZK6_BACFR	Q64zk6 bacteroides
302	7	0.9	273	2	Q620W7_ORYSA	Q620w7 oryza sativ
303	7	0.9	274	2	Q50VM4_ENTHI	Q50vm4 entamoeba h
304	7	0.9	274	2	Q4IVD6_AZOVI	Q4ivd6 azotobacter
305	7	0.9	274	2	Q87KK2_VIBPA	Q87kk2 vibrio para
306	7	0.9	277	2	Q4PHA7_USTMA	Q4pha7 usilago ma
307	7	0.9	277	2	Q7YZT2_TRYCO	Q7yzt2 trypanosoma
308	7	0.9	277	2	Q5WP13_9BRAD	Q5wp13 bradyrhizob
309	7	0.9	277	2	Q5WP11_9BRAD	Q5wp11 bradyrhizob
310	7	0.9	278	2	Q4WNH5_ASPFU	Q4wnh5 aspergillus
311	7	0.9	279	2	Q758X7_ASHGO	Q758x7 ashbya gos
312	7	0.9	279	2	Q6P3A1_MOUSE	Q6p3a1 mus musculu
313	7	0.9	280	1	CBIO1_STRF3	Q79y7 streptococc
314	7	0.9	280	1	CBIO1_STRF6	Q5x9b6 streptococc
315	7	0.9	280	1	CBIO1_STRP8	Q7cmm8 streptococc
316	7	0.9	280	1	CBIO1_STRPV	Q99x12 streptococc
317	7	0.9	280	2	Q5UTN3_HALMA	Q5utn3 haloarcula
318	7	0.9	280	2	P90872_CAEL	P90872 caenorhabdi
319	7	0.9	280	2	Q9ABA2_CAUCR	Q9aba2 caulobacter
320	7	0.9	281	2	Q8DUM0_STRMU	Q8dum0 streptococc
321	7	0.9	282	2	Q96NE7_HUMAN	Q96ne7 homo sapien
322	7	0.9	283	2	Q9RJF9_STRCO	Q9rf9 streptomyc
323	7	0.9	287	1	PSA3_YEAST	P21242 saccharomyc

324	7	0.9	288	2	Q8W190_EUGGR	Q8w190 euglena gra
325	7	0.9	288	2	Q823B6_CHLCV	Q823b6 chlamydophi
326	7	0.9	289	2	Q743L1_MYCPA	Q743l1 mycobacteri
327	7	0.9	290	2	Q749Y5_GEOSL	Q749y5 geobacter s
328	7	0.9	291	2	Q615Z1_CAEBR	Q615z1 caenorhabdi
329	7	0.9	291	2	Q30441_BORPE	Q30441 bordetella
330	7	0.9	291	2	Q7W3M9_BORPA	Q7w3m9 bordetella
331	7	0.9	291	2	Q7WF05_BORBR	Q7wf05 bordetella
332	7	0.9	292	2	Q5LY08_MAGGR	Q5ly08 magnaporthe
333	7	0.9	292	2	Q9REA4_ENTFA	Q9rea4 enterococcu
334	7	0.9	292	2	Q5TRH6_ANOGA	Q5trh6 anopheles g
335	7	0.9	295	2	Q9GL75_BOVIN	Q9gl75 bos taurus
336	7	0.9	295	2	Q9ERF5_MESAU	Q9erf5 mesocricetu
337	7	0.9	296	2	Q4IQE4_GIBZE	Q4iqe4 gibberella
338	7	0.9	297	2	Q7SG71_NEUCR	Q7sg71 neurospora
339	7	0.9	298	2	Q5B0V7_EMENI	Q5b0v7 aspergillus
340	7	0.9	298	2	Q9GL74_CERAE	Q9gl74 cercopithe
341	7	0.9	298	2	Q7M9T0_WOLSU	Q7m9t0 wolinnella s
342	7	0.9	299	2	Q7QPM1_GIALA	Q7qpm1 giardia lam
343	7	0.9	299	2	Q8D4T3_VIBVU	Q8d4t3 vibrio vuln
344	7	0.9	301	2	Q7MGD6_VIBVU	Q7mgd6 vibrio vuln
345	7	0.9	301	2	Q8PXU9_METMA	Q8pxu9 methanosarc
346	7	0.9	301	2	Q82B65_STRAW	Q82b65 streptomyc
347	7	0.9	304	2	Q8FRS6_COREF	Q8frs6 corynebacte
348	7	0.9	305	2	Q6APE9_DESPA	Q6ape9 desulfotale
349	7	0.9	305	2	Q7RUI7_NEUCR	Q7rui7 neurospora
350	7	0.9	306	2	Q8UCH5_AGRTS	Q8uch5 agrobacteri
351	7	0.9	306	2	Q61W15_CAEBR	Q61w15 caenorhabdi
352	7	0.9	307	2	Q8LCAZ_ARATH	Q8lcaz arabidopsis
353	7	0.9	308	2	Q84L58_ECICAR	Q84l58 cicer ariet
354	7	0.9	308	2	Q8FCP5_ECOL6	Q8fcp5 escherichia
355	7	0.9	308	2	Q828C9_STRAW	Q828c9 streptomyc
356	7	0.9	311	2	Q4JUC2_CORJK	Q4juc2 corynebacte
357	7	0.9	311	2	Q8U9T2_AGRTS	Q8u9t2 agrobacteri
358	7	0.9	312	2	Q60K08_CAEBR	Q60k08 caenorhabdi
359	7	0.9	312	2	Q5FS46_GLUOX	Q5fs46 gluconobact
360	7	0.9	313	2	Q4NV47_9DELTA	Q4nv47 anaeromyxob
361	7	0.9	314	2	Q8LG78_ARATH	Q8lg78 arabidopsis
362	7	0.9	314	2	Q9LPG3_ARATH	Q9lp92 arabidopsis
363	7	0.9	315	2	Q55KJ9_CRYNE	Q55kj9 cryptococcu
364	7	0.9	315	2	Q5KAY2_CRYNE	Q5kay2 cryptococcu
365	7	0.9	315	2	Q9FVX5_ARATH	Q9fvx5 arabidopsis
366	7	0.9	316	2	Q82W49_NITEU	Q82w49 nitrosomona
367	7	0.9	316	2	Q65566_9ALPH	Q65566 bovine herp
368	7	0.9	316	2	Q77CC0_9ALPH	Q77cc0 bovine herp
369	7	0.9	317	2	Q7N4V6_PHOLL	Q7n4v6 photorhabdu
370	7	0.9	317	2	Q6N9N0_RHOPA	Q6n9n0 rhodospseudo
371	7	0.9	320	1	FLAA1_TREHY	P32520 treponema h
372	7	0.9	322	2	Q6H4W3_ORYSA	Q6h4w3 oryza sativ
373	7	0.9	324	2	Q57SJ2_SALCH	Q57sj2 salmonella
374	7	0.9	324	2	Q5PFX0_SALPA	Q5pf0 salmonella
375	7	0.9	324	2	Q7CR48_SALTY	Q7cr48 salmonella
376	7	0.9	324	2	Q8XGHO_SALTI	Q8xgho salmonella
377	7	0.9	325	2	Q9P753_NEUCR	Q9p753 neurospora
378	7	0.9	325	2	Q9FAA4_9CORY	Q9faa4 brevivibacter
379	7	0.9	325	2	Q4KJT7_PSEF5	Q4kjt7 pseudomonas
380	7	0.9	325	2	Q79VGS_CORGL	Q79vg6 corynebacte
381	7	0.9	325	2	Q6NHT0_CORDI	Q6nht0 corynebacte
382	7	0.9	326	2	Q6NHT0_CORDI	Q6nht0 corynebacte
383	7	0.9	326	2	Q5RKJ0_RAT	Q5rkj0 rattus norv
384	7	0.9	326	2	Q6NQC3_ARATH	Q6nqc3 arabidopsis
385	7	0.9	328	2	Q9RB11_PSCCC	Q9rb11 pectobacter
386	7	0.9	328	2	Q7USN3_RHOBA	Q7usn3 rhodospirell
387	7	0.9	329	2	Q5N9N9_CANAL	Q5n9n9 candida alb
388	7	0.9	329	2	Q4JVK6_CORJK	Q4jvk6 corynebacte
389	7	0.9	329	2	Q4RB11_TETNG	Q4rb11 tetraodon n
390	7	0.9	330	2	Q5N78_CANAL	Q5n78 candida alb
391	7	0.9	330	2	Q7U9S8_SYNXP	Q7u9s8 synchococc
392	7	0.9	331	2	Q71118_9HIV1	Q71118 human immun
393	7	0.9	332	2	Q5ATH3_EMENI	Q5ath3 aspergillus
394	7	0.9	332	2	Q5N2U1_SYNPE	Q5n2u1 synchococc
395	7	0.9	333	2	Q4I337_GIBZE	Q4i337 gibberella

397	7	0.9	333	2	Q88VL6_LACPL	Q88VL6 lactobacill	470	7	0.9	360	2	Q5JP96_HUMAN	Q5JP96 homo sapien
398	7	0.9	335	2	Q9ZPW3_ARATH	Q9ZPW3 arabidopsis	471	7	0.9	360	2	Q54MCS_DICDI	Q54MCS dictyosteli
399	7	0.9	335	2	Q71115_9HIV1	Q71115 human immun	472	7	0.9	360	2	Q8D7X9_VIBVU	Q8D7X9 vibrio vuln
400	7	0.9	335	2	Q71116_9HIV1	Q71116 human immun	473	7	0.9	360	2	Q7MEZ5_VIBVU	Q7MEZ5 vibrio vuln
401	7	0.9	335	2	Q71117_9HIV1	Q71117 human immun	474	7	0.9	361	2	Q6L1J2_PICTO	Q6L1J2 picitrophilus
402	7	0.9	335	2	Q71120_9HIV1	Q71120 human immun	475	7	0.9	361	2	Q82WK0_NITEU	Q82WK0 nitrosomona
403	7	0.9	335	2	Q71320_9HIV1	Q71320 human immun	476	7	0.9	362	1	LDOX_VITVI	P51093 vitis vinif
404	7	0.9	336	1	KCNK1_MOUSE	Q8581 mus musculus	477	7	0.9	362	1	RECA_BRAJA	Q85814 bradyrhizob
405	7	0.9	336	1	OTCC_STRP3	P65609 streptococc	478	7	0.9	362	2	Q8T114_PHYPO	Q8T114 physarum po
406	7	0.9	336	1	OTCC_STRP6	Q5XAV4 streptococc	479	7	0.9	362	2	Q73V31_MYCPA	Q73V31 mycobacteri
407	7	0.9	336	1	OTCC_STRP8	P65610 streptococc	480	7	0.9	362	2	Q6GN23_XENLA	Q6GN23 xenopus lae
408	7	0.9	336	1	OTCC_STRPY	P16964 streptococc	481	7	0.9	363	1	LEU3A_ASPNG	P87256 aspergillus
409	7	0.9	336	1	Q99L39_MOUSE	Q99L39 mus musculus	482	7	0.9	363	2	Q60WN7_CABER	Q60WN7 caenorhabdi
410	7	0.9	337	1	GIMA2_HUMAN	Q9U222 homo sapien	483	7	0.9	364	2	Q877A9_ASPOR	Q877A9 aspergillus
411	7	0.9	337	1	OTCC2_STRA3	P65605 streptococc	484	7	0.9	364	2	Q52GH3_MAGGR	Q52GH3 magnaporthe
412	7	0.9	337	1	OTCC2_STRA5	P65606 streptococc	485	7	0.9	366	2	Q5BEW8_EMENI	Q5BEW8 aspergillus
413	7	0.9	337	1	OTCC_STRAG	Q8RP83 streptococc	486	7	0.9	366	2	Q4WRM6_ASPFU	Q4WRM6 aspergillus
414	7	0.9	337	1	OSRCT2_PONPY	Q5RC12 pongo pygma	487	7	0.9	367	2	Q60B60_METCA	Q60B60 methylococc
415	7	0.9	337	2	QARPS3_TETNG	QARPS3 tetraodon n	488	7	0.9	367	2	Q98G12_RHILO	Q98G12 rhizobium l
416	7	0.9	339	2	Q4WEN6_ASPFU	Q4WEN6 aspergillus	489	7	0.9	369	2	Q5YM04_ORYSA	Q5YM04 o hyppotheti
417	7	0.9	339	2	Q5DMW2_ARATH	Q5DMW2 arabidopsis	490	7	0.9	369	2	Q524G5_ORYSA	Q524G5 oryza sativ
418	7	0.9	339	2	Q8C9Y2_MOUSE	Q8C9Y2 mus musculus	491	7	0.9	369	2	Q5Z4H4_ORYSA	Q5Z4H4 oryza sativ
419	7	0.9	340	2	Q9G644_9SAUR	Q9G644 calotes cal	492	7	0.9	369	2	Q7ZWM8_XENLA	Q7ZWM8 xenopus lae
420	7	0.9	341	2	Q5KMW9_GEOKA	Q5KMW9 geobacillus	493	7	0.9	370	2	Q4Q7Z3_LEIMA	Q4Q7Z3 leishmania
421	7	0.9	341	2	Q98CD7_RHILO	Q98CD7 rhizobium l	494	7	0.9	370	2	Q27855_TETTH	Q27855 tetrahymena
422	7	0.9	341	2	Q7UJB2_RHOBA	Q7UJB2 rhodopirell	495	7	0.9	371	2	Q73RV5_MYCPA	Q73RV5 mycobacteri
423	7	0.9	342	1	OST6_HUMAN	Q96q15 homo sapien	496	7	0.9	371	2	Q8FR78_COREF	Q8FR78 corynebacte
424	7	0.9	342	2	Q5H9K7_HUMAN	Q5H9K7 homo sapien	497	7	0.9	371	2	Q6R796_9HERP	Q6R796 oreitred her
425	7	0.9	343	1	Q5YV31_NOCFA	Q5YV31 nocardia fa	498	7	0.9	373	1	SECU_YEAST	P40316 saccharomyc
426	7	0.9	344	1	RNF2_XENLA	Q66169 xenopus lae	499	7	0.9	374	2	Q4XX42_PLACH	Q4XX42 plasmodium
427	7	0.9	344	2	Q4WXG1_ASPFU	Q4WXG1 aspergillus	500	7	0.9	375	1	RECA_RHOBA	Q7UJ10 rhodopirell
428	7	0.9	344	2	Q9X6Q6_ACTPL	Q9X6Q6 actinobacil	501	7	0.9	375	2	Q708E2_9CAUD	Q708E2 bactariopha
429	7	0.9	344	2	Q4IYW1_AZOVI	Q4IYW1 azotobacter	502	7	0.9	376	2	Q76L01_9CILI	Q76L01 dileptus ma
430	7	0.9	344	2	Q630X0_BACC2	Q630X0 bacillus ce	503	7	0.9	376	2	Q7WZC5_LACJO	Q7WZC5 lactobacill
431	7	0.9	345	2	Q6P164_HUMAN	Q6P164 homo sapien	504	7	0.9	377	1	RING1_CANFA	Q5TJF3 canis famil
432	7	0.9	346	1	ETFL_CRYNE	Q810w1 cryptococcu	505	7	0.9	377	1	RING1_HUMAN	Q06587 homo sapien
433	7	0.9	346	2	Q5DAI8_SCHJA	Q5DAI8 schistosoma	506	7	0.9	377	1	RING1_MACMU	Q8WMU5 macaca mula
434	7	0.9	346	2	Q3REP7_PONPY	Q3REP7 pongo pygma	507	7	0.9	377	2	Q35730_MOUSE	Q35730 mus musculu
435	7	0.9	347	2	Q9SU74_ARATH	Q9SU74 arabidopsis	508	7	0.9	377	2	Q6MGB6_RAT	Q6MGB6 rattus norv
436	7	0.9	347	2	Q8SH97_BROPE	Q8SH97 brookesia p	509	7	0.9	377	2	Q921Z8_MOUSE	Q921Z8 mus musculu
437	7	0.9	347	2	Q8SHA3_BROBR	Q8SHA3 brookesia b	510	7	0.9	377	2	Q4FK33_MOUSE	Q4FK33 mus musculu
438	7	0.9	348	2	Q52EH4_MAGGR	Q52EH4 magnaporthe	511	7	0.9	377	2	Q8AV27_CHICK	Q8AV27 gallus gall
439	7	0.9	348	2	Q8REG8_NOCA	Q8REG8 rhodococcus	512	7	0.9	379	2	Q57G04_BRUAB	Q57G04 brucella ab
440	7	0.9	348	2	Q70PA6_9DELT	Q70PA6 melittangiu	513	7	0.9	379	2	Q8G3E1_BRUSU	Q8G3E1 brucella su
441	7	0.9	348	2	Q5LBF9_BACFN	Q5LBF9 bacteroides	514	7	0.9	380	2	Q9KYW7_STRCO	Q9KYW7 streptomyce
442	7	0.9	348	2	Q64R21_BACFR	Q64R21 bacteroides	515	7	0.9	380	2	Q8YEE1_BRUME	Q8YEE1 brucella me
443	7	0.9	349	1	ISPG_CLOAB	Q97156 clostridium	516	7	0.9	381	2	Q4UEE8_THEAN	Q4UEE8 theileria a
444	7	0.9	349	2	Q51A59_ENTHI	Q51A59 entamoeba h	517	7	0.9	382	2	Q5P656_AZOSE	Q5P656 azoarcus sp
445	7	0.9	349	2	Q8CFE7_MOUSE	Q8CFE7 mus musculu	518	7	0.9	382	2	Q7MT14_PORGI	Q7MT14 porphyromon
446	7	0.9	351	2	Q66K46_HUMAN	Q66K46 homo sapien	519	7	0.9	382	2	Q5YXR8_NOCFA	Q5YXR8 nocardia fa
447	7	0.9	351	2	Q70AX1_ACTTI	Q70AX1 actinoplane	520	7	0.9	382	2	Q6NWD4_ERARE	Q6NWD4 brachydanio
448	7	0.9	351	2	Q6AL26_DESPS	Q6AL26 desulfofale	521	7	0.9	383	2	Q8KWF1_BACST	Q8KWF1 bacillus st
449	7	0.9	351	2	Q6NS95_MOUSE	Q6NS95 mus musculu	522	7	0.9	383	2	Q6UD24_9PROT	Q6UD24 uncultured
450	7	0.9	352	2	Q5BCCG1_EMENI	Q5BCCG1 aspergillus	523	7	0.9	383	2	Q6UD50_9PROT	Q6UD50 uncultured
451	7	0.9	353	2	Q4R617_WACPA	Q4R617 macaca fasc	524	7	0.9	383	2	Q63IN7_BURPS	Q63IN7 burkholderi
452	7	0.9	353	2	Q6Z2G5_ACTTI	Q6Z2G5 actinoplane	525	7	0.9	383	2	Q8NR26_CORGL	Q8NR26 corynebacte
453	7	0.9	353	2	Q5YT17_NOCFA	Q5YT17 nocardia fa	526	7	0.9	384	2	Q9FSQ3_ORYSA	Q9FSQ3 oryza sativ
454	7	0.9	354	2	Q99XC6_STAAN	Q99XC6 staphylococ	527	7	0.9	384	2	Q40492_TOBAC	Q40492 nicotiana t
455	7	0.9	355	1	PHBC_CHRVI	P45370 c poly-beta	528	7	0.9	384	2	Q921J4_RHIME	Q921J4 rhizobium m
456	7	0.9	355	2	Q9C778_ARATH	Q9C778 arabidopsis	529	7	0.9	385	2	Q8TRZ1_METAC	Q8TRZ1 methanosaar
457	7	0.9	355	2	Q4W0V9_ARATH	Q4W0V9 arabidopsis	530	7	0.9	385	2	Q5YXD4_NOCFA	Q5YXD4 nocardia fa
458	7	0.9	355	2	Q31252_NOST	Q31252 anabaena sp	531	7	0.9	386	2	Q7VS16_EORFE	Q7VS16 bordetella
459	7	0.9	355	2	Q6GD41_STAAS	Q6GD41 staphylococ	532	7	0.9	386	2	Q7WEB8_EORBR	Q7WEB8 bordetella
460	7	0.9	355	2	Q5HJT9_STAAC	Q5HJT9 staphylococ	533	7	0.9	387	1	RECA_LEPBI	P48290 leptospira
461	7	0.9	355	2	Q7NK07_GLOVI	Q7NK07 gloeobacter	534	7	0.9	387	2	Q6PFK0_BRARE	Q6PFK0 brachydanio
462	7	0.9	355	2	Q8NVY5_STAAM	Q8NVY5 staphylococ	535	7	0.9	388	1	XYLA_STRCK	Q9S324 streptomyce
463	7	0.9	355	2	Q8YVAL_ANASP	Q8YVAL anabena sp	536	7	0.9	388	2	Q4NLG9_9MICC	Q4NLG9 arthrobacte
464	7	0.9	357	2	Q7NZ09_CHRVO	Q7NZ09 chromobacte	537	7	0.9	390	2	Q8PV83_METNA	Q8PV83 methanosaar
465	7	0.9	358	1	RECA2_MYXXA	P48292 myxococcus	538	7	0.9	390	2	Q9LIV7_ARATH	Q9LIV7 arabidopsis
466	7	0.9	358	2	Q4Q699_LEIMA	Q4Q699 leishmania	539	7	0.9	390	2	Q4NE55_9MICC	Q4NE55 arthrobacte
467	7	0.9	358	2	Q4NPR7_9DELT	Q4NPR7 anaeromyxob	540	7	0.9	390	2	Q5WHZ3_BACSK	Q5WHZ3 bacillus cl
468	7	0.9	358	2	Q81PE1_BACAN	Q81PE1 bacillus an	541	7	0.9	391	2	Q8T3J1_DROME	Q8T3J1 drosophila
469	7	0.9	358	2	Q7S255_BRARE	Q7S255 brachydanio	542	7	0.9	392	2	Q4YS02_PLABE	Q4YS02 plasmodium



543	7	0.9	392	2	Q4MRB9_BACCE	Q4mh9 bacillus ce	616	7	0.9	428	2	Q747R9_GEOSL	Q747r9 geobacter s
544	7	0.9	393	2	Q7RS78_PLAYO	Q7rst8 plasmodium	617	7	0.9	429	1	SYS_PHOLL	Q7nce7 photorhabdu
545	7	0.9	393	2	Q5KV50_GEOKA	Q5kv50 geobacillus	618	7	0.9	429	7	Q8YCL3_BRUME	Q8ycl3 brucella me
546	7	0.9	393	2	Q65F04_BACLD	Q65f04 bacillus l1	619	7	0.9	430	2	Q7RAW2_PLAYO	Q7raw2 plasmodium
547	7	0.9	394	2	Q8IK92_PLAF7	Q8ik92 plasmodium	620	7	0.9	431	2	Q21194_CABEL	Q21194 caenorhabdi
548	7	0.9	394	2	Q9R672_SYNPF	Q9r6t2 synechococc	621	7	0.9	431	2	Q8HT85_9TRAC	Q8ht85 selaginella
549	7	0.9	394	2	Q6HXK4_BACAN	Q6hxx4 bacillus an	622	7	0.9	431	2	Q73M29_TREDE	Q73m29 treponema d
550	7	0.9	394	2	Q5LVC8_SILPO	Q5lvc8 silicibacte	623	7	0.9	431	2	Q66H32_RAT	Q66h32 rattus norv
551	7	0.9	397	2	Q4HZ87_GIBZE	Q4hz87 gibberella	624	7	0.9	432	2	Q5AZG5_EMENI	Q5azg5 aspergillus
552	7	0.9	397	2	Q5DWM4_ARATH	Q5dwm4 arabidopsis	625	7	0.9	432	2	Q4KCI5_PSEF5	Q4kci5 pseudomonas
553	7	0.9	398	2	Q89E17_BRAJA	Q89e17 bradyrhizob	626	7	0.9	432	2	Q6NWF0_BRARE	Q6nwf0 brachydanio
554	7	0.9	399	1	ENO_ARCFU	Q291133 archaeoglob	627	7	0.9	433	2	Q4HAM9_9DEIO	Q4ham9 deinococcus
555	7	0.9	401	2	Q5B621_EMENI	Q5b621 aspergillus	628	7	0.9	434	2	Q5ASG9_EMENI	Q5asg9 aspergillus
556	7	0.9	401	2	Q911P8_PSEAE	Q91lp8 pseudomonas	629	7	0.9	435	2	Q9TXJ4_LEIMA	Q9txj4 leishmania
557	7	0.9	402	2	Q5FLB1_LACAC	Q5fle1 lactobacill	630	7	0.9	435	2	Q6G2S5_BARHE	Q6g2s5 bartonella
558	7	0.9	402	2	Q8ET06_OCEIH	Q8et06 oceanobacil	631	7	0.9	436	2	Q836C0_ENTFA	Q836c0 enterococcu
559	7	0.9	404	2	Q6BGH7_PABCT	Q6bgi7 paramecium	632	7	0.9	437	2	Q4K3C1_PSEF5	Q4k3c1 pseudomonas
560	7	0.9	404	2	Q6SH30_9BACT	Q6sh30 uncultured	633	7	0.9	437	2	Q6D2L6_ERWCT	Q6d2l6 erwinia car
561	7	0.9	405	2	Q9NV04_HUMAN	Q9nv04 homo sapien	634	7	0.9	437	2	Q6BCG8_EDWIC	Q6bcg8 edwardsiell
562	7	0.9	406	2	Q86V19_HUMAN	Q86v19 homo sapien	635	7	0.9	438	2	Q4ROX6_TETNG	Q4rox6 tetraodon n
563	7	0.9	406	2	Q5TJF4_CANFA	Q5tjf4 canis famil	636	7	0.9	439	2	Q4Q698_LEIMA	Q4q698 leishmania
564	7	0.9	406	2	Q4KMC1_RAT	Q4kmc1 rattus norv	637	7	0.9	440	2	Q4TAU6_TETNG	Q4tau6 tetraodon n
565	7	0.9	407	2	Q5PXG6_SPOSC	Q5pxg6 sporothrix	638	7	0.9	441	2	Q4WC28_ASPFU	Q4wc28 aspergillus
566	7	0.9	407	2	Q6YPE8_ORISA	Q6ype8 oryza sativ	639	7	0.9	442	2	Q5GUF1_XANOR	Q5guf1 xanthomonas
567	7	0.9	408	2	Q6CMJ5_KIULA	Q6cmj5 kluyveromyc	640	7	0.9	442	2	Q5NTF9_9BACT	Q5ntf9 uncultured
568	7	0.9	409	1	PRX12_FICPA	Q01961 pichia past	641	7	0.9	443	2	Q23497_CABEL	Q23497 caenorhabdi
569	7	0.9	410	2	Q51L21_MAGGR	Q51l21 magnaporthe	642	7	0.9	444	2	Q89M95_BRAJA	Q89m95 bradyrhizob
570	7	0.9	410	2	Q51F48_ENTHI	Q51f48 entamoeba h	643	7	0.9	444	2	Q89NW0_BRAJA	Q89nw0 bradyrhizob
571	7	0.9	410	2	Q4Q1S8_LEIMA	Q4q1s8 leishmania	644	7	0.9	445	2	Q4HRF7_CAMUP	Q4hrf7 campylobact
572	7	0.9	410	2	Q6E2R6_STRAJ	Q6e2r6 streptococc	645	7	0.9	445	2	Q6N715_RHOPA	Q6n715 rhodospseudo
573	7	0.9	410	2	Q6AB18_PROAC	Q6ab18 propionibac	646	7	0.9	446	2	Q7SB26_NEUCR	Q7sb26 neuropora
574	7	0.9	411	2	Q5NPX0_ZYMMO	Q5npx0 zymononas m	647	7	0.9	446	2	Q6BU59_DEBHA	Q6bu59 debaryomyce
575	7	0.9	412	2	Q580B2_9TRYP	Q580b2 trypanosoma m	648	7	0.9	448	2	Q5J361_PYRKO	Q5j361 pyrococcus
576	7	0.9	412	2	Q92575_ZYMMO	Q925t5 zymononas m	649	7	0.9	451	1	Q8Y1V0_BALSO	Q8y1v0 kalsstonia s
577	7	0.9	412	2	Q4IV81_AZOV1	Q4iv81 azotobacter	650	7	0.9	451	1	VPS9_YEAST	Q34787 saccharomyc
578	7	0.9	413	2	Q96125_HUMAN	Q96125 homo sapien	651	7	0.9	453	2	Q6A855_PROAC	Q6a855 propionibac
579	7	0.9	413	2	Q5JSN8_HUMAN	Q5jsn8 homo sapien	652	7	0.9	455	2	Q5A418_CANAL	Q5a418 candida alb
580	7	0.9	413	2	Q5E7Q7_VIBF1	Q5e7q7 vibrio fisc	653	7	0.9	456	2	Q57794_PYROCOC	Q57794 pyrococcus
581	7	0.9	413	2	Q8JZV4_MOUSE	Q8jzv4 m riken cdn	654	7	0.9	456	2	Q7QB46_ANOGA	Q7qb46 anopheles g
582	7	0.9	414	1	CDC61_METAC	Q8tur2 methanosarc	655	7	0.9	456	2	Q8R9H8_TETYN	Q8r9h8 thermocanae
583	7	0.9	414	1	CDC61_METWA	Q8pxa8 methanosarc	656	7	0.9	459	2	Q881M9_PSESM	Q881m9 pseudomonas
584	7	0.9	415	1	CDC6_PYRKO	Q5jet2 pyrococcus	657	7	0.9	460	2	Q98RZ3_GUITH	Q98rz3 guillardia
585	7	0.9	415	1	PGK_ASHGO	Q757q0 ashbya goss	658	7	0.9	460	2	Q74GQ7_GEOSL	Q74gq7 geobacter s
586	7	0.9	416	2	Q6GCU8_STAAS	Q6gcu8 staphylococ	659	7	0.9	461	2	Q6JKE9_NUCL	Q6jke9 neodiprion
587	7	0.9	416	2	Q6GKCB_STAAR	Q6gkcb staphylococ	660	7	0.9	462	2	Q57ZN8_9TRYP	Q57zn8 trypanosoma
588	7	0.9	416	2	Q5HJ35_STAAC	Q5hj35 staphylococ	661	7	0.9	463	2	Q41LH4_GIBZE	Q41lh4 gibberella
589	7	0.9	416	2	Q7A1Y3_STAAN	Q7a1y3 staphylococ	662	7	0.9	463	2	Q6SY98_PHOLU	Q6sy98 photorhabdu
590	7	0.9	416	2	Q7A814_STAAN	Q7a814 staphylococ	663	7	0.9	464	2	Q723Y7_HUMAN	Q723y7 homo sapien
591	7	0.9	416	2	Q99X43_STAAM	Q99x43 staphylococ	664	7	0.9	466	2	Q5DBX8_SCHJA	Q5dbx8 schistosoma
592	7	0.9	417	1	PGK_CANMA	P41757 candida mal	665	7	0.9	466	2	Q579C6_BRUAB	Q579c6 brucella ab
593	7	0.9	418	2	Q41FL6_GIBZE	Q41fl6 gibberella	666	7	0.9	466	2	Q8FVD7_BRUSU	Q8fvd7 brucella su
594	7	0.9	418	2	Q8DMW5_STRAS	Q8dmw5 streptococc	667	7	0.9	466	2	Q4H6R7_9DEIO	Q4h6r7 deinococcus
595	7	0.9	419	1	CDC6_PYRAB	Q9v2f2 pyrococcus	668	7	0.9	469	2	Q51997_HALSA	Q51997 halobacteri
596	7	0.9	419	1	CDC6_PYRHO	Q57864 pyrococcus	669	7	0.9	469	2	Q6CSM6_KIULA	Q6csm6 kluyveromyc
597	7	0.9	419	1	Y4ML_RHISN	P55571 rhizobium s	670	7	0.9	469	2	Q4IBZ4_GIBZE	Q4ibz4 gibberella
598	7	0.9	419	2	Q4WBZ3_ASPFU	Q4wbz3 aspergillus	671	7	0.9	470	2	Q6AF02_LEIXX	Q6af02 leifsonia x
599	7	0.9	420	1	CDC6_PYRFU	P81413 pyrococcus	672	7	0.9	471	2	Q9EZK6_STRPY	Q9ezk6 streptococc
600	7	0.9	420	1	Y1541_METJA	Q89j36 methanococc	673	7	0.9	471	2	Q9RCK6_STRPY	Q9rck6 streptomyce
601	7	0.9	420	1	Q9RJQ6_STRCO	Q9rjq6 streptomyce	674	7	0.9	472	2	Q92CE1_LISIN	Q92cel listeria in
602	7	0.9	421	2	Q5TPJ5_ANOGA	Q5tpj5 anopheles g	675	7	0.9	472	2	Q9F2B6_THAAR	Q9f2b6 thauera aro
603	7	0.9	421	2	Q95V69_TETTH	Q95v69 tetrahymena	676	7	0.9	472	2	DNAA_PORGI	Q7mx21 porphyromon
604	7	0.9	422	1	LACE_AGRRD	P29822 agrobacteri	677	7	0.9	473	1	DNAA_PORGI	Q7mx21 porphyromon
605	7	0.9	422	2	Q5BHU6_DROME	Q5bhu6 drosophila	678	7	0.9	473	2	Q71211_STRTE	Q71211 streptomyce
606	7	0.9	422	2	Q57LY9_SALCH	Q57ly9 salmonella	679	7	0.9	473	2	Q84142_RACTO	Q84142 streptomyce
607	7	0.9	422	2	Q5PCV3_SALPA	Q5pcv3 salmonella	680	7	0.9	475	2	Q6Y636_MOUSE	Q6y636 mus musculus
608	7	0.9	422	2	Q82NC0_SALTY	Q8nc0 salmonella	681	7	0.9	476	2	Q41695_GIBZE	Q41695 agrobacteri
609	7	0.9	423	2	Q5RBEZ_PONPY	Q5rbz5 pongo pygma	682	7	0.9	476	2	Q8U552_AGRT5	Q8u552 agrobacteri
610	7	0.9	423	2	Q93256_CHICK	Q93256 gallus gall	683	7	0.9	477	2	Q7V9V6_PROMA	Q7v9v6 prochloroc
611	7	0.9	424	2	Q89R42_BRAJA	Q89r42 bradyrhizob	684	7	0.9	477	2	Q87HT2_VTBPA	Q87ht2 vibrio para
612	7	0.9	427	2	Q4HL64_CAMLA	Q4hl64 campylobact	685	7	0.9	478	2	Q4S8J0_TETNG	Q4s8j0 tetraodon n
613	7	0.9	428	2	Q60947_TRYCR	Q60947 trypanosoma	686	7	0.9	480	2	Q6R2R8_9VIRU	Q6r2r8 hyposoter d
614	7	0.9	428	2	Q5R891_PONPY	Q5r891 pongo pygma	687	7	0.9	481	2	Q7Q2A3_ANOGA	Q7q2a3 anopheles g
615	7	0.9	428	2	P74349_SYN93	P74349 synechocyst	688	7	0.9	482	2	Q892C7_CLOTE	Q892c7 clostridium

589	7	0.9	483	2	Q531B6_STRGR	Q531b6 streptomyc	762	7	0.9	546	2	Q7UT65_RHOBA	Q7ut65 rhodopirell
590	7	0.9	485	2	Q4Q263_LEIMA	Q4q263 leishmania	763	7	0.9	547	2	Q7SAW8_ASHGO	Q7SAW8 ashbya goss
591	7	0.9	485	2	Q6W1U7_RHIZOB	Q6w1u7 rhizobium s	764	7	0.9	547	2	Q8AIJ6_BACTN	Q8aij6 bacteroides
592	7	0.9	485	2	Q731L4_TREDE	Q731l4 treponema d	765	7	0.9	547	2	Q7J378_TREDE	Q7j378 treponema d
593	7	0.9	486	2	Q62P84_HUMAN	Q62p84 homo sapien	766	7	0.9	549	2	Q4NU97_9DELT	Q4nu97 anaeromyxob
594	7	0.9	487	2	Q8U0H5_PYRTU	Q8u0h5 pyrococcus	767	7	0.9	549	2	Q4NUZ1_9DELT	Q4nuz1 anaeromyxob
595	7	0.9	487	2	Q578Q5_BRUAB	Q578q5 brucella ab	768	7	0.9	550	2	Q9RB11_AC1AD	Q9rb11 acinetobact
596	7	0.9	487	2	Q7SXF3_BRARE	Q7sxf3 brachydanio	769	7	0.9	550	2	Q6FCC3_AC1AD	Q6fcc3 acinetobact
597	7	0.9	488	2	Q6PJJ6_HUMAN	Q6pj16 homo sapien	770	7	0.9	551	2	Q6J9V5_MAIZE	Q6j9v5 zea mays (m
598	7	0.9	488	2	Q524G6_ORYSA	Q524g6 oryza sativ	771	7	0.9	556	2	Q5B706_EMENI	Q5b706 aspergillus
599	7	0.9	488	2	Q528M4_ORYSA	Q528m4 oryza sativ	772	7	0.9	556	2	Q810A1_MOUSE	Q810a1 mus musculus
700	7	0.9	488	2	Q8SB18_ORYSA	Q8eb18 oryza sativ	773	7	0.9	556	2	Q9D972_MOUSE	Q9d972 mus musculus
701	7	0.9	488	2	Q5YM05_ORYSA	Q5ym05 o. hypotheti	774	7	0.9	562	1	CH60_TREYCR	Q95046 trypanosoma
702	7	0.9	488	2	Q89H76_BRAJA	Q89h76 bradyrhizob	775	7	0.9	562	2	Q8NK91_ASFOR	Q8nk91 aspergillus
703	7	0.9	489	1	CP128_MYCBO	P63714 mycobacteri	776	7	0.9	562	2	Q7SAY9_ASHGO	Q7SAy9 ashbya goss
704	7	0.9	489	1	CP128_MYCTU	P63713 mycobacteri	777	7	0.9	562	2	Q9V725_DROME	Q9v725 drosophila
705	7	0.9	489	1	OC1N_POTTR	Q82793 potorosus tr	778	7	0.9	562	2	Q4Q1M0_LEIMA	Q4q1m0 leishmania
706	7	0.9	490	2	Q54WV0_DICDI	Q54wv0 dictyosteli	779	7	0.9	564	2	Q9PQT6_UREPA	Q9pqt6 ureaplasma
707	7	0.9	491	2	Q5LYN0_STR11	Q5lyn0 streptococc	780	7	0.9	567	2	Q9HGH9_ASFOR	Q9hgh9 aspergillus
708	7	0.9	491	2	Q5M393_STR12	Q5m393 streptococc	781	7	0.9	568	2	Q59WU0_CANAL	Q59wu0 candida alb
709	7	0.9	493	2	Q761Y0_ORYSA	Q761y0 oryza sativ	782	7	0.9	568	2	Q524M2_MAGGR	Q524m2 magnaporthe
710	7	0.9	497	2	Q8DQ91_STR16	Q8dq91 streptococc	783	7	0.9	572	2	Q6ZH86_ORYSA	Q6zh86 oryza sativ
711	7	0.9	497	2	Q97RD6_STRPN	Q97rd6 streptococc	784	7	0.9	573	2	Q9VDS0_DROME	Q9vds0 drosophila
712	7	0.9	498	2	Q97V40_SULSO	Q97v40 sulfolobus	785	7	0.9	575	2	Q651P7_BACLD	Q651p7 bacillus li
713	7	0.9	498	2	Q6X195_9CAUD	Q6x195 bacterioph	786	7	0.9	578	2	Q5GH49_FUGRU	Q5gh49 fugu rubrip
714	7	0.9	499	2	Q6X1A1_9CAUD	Q6x1a1 bacterioph	787	7	0.9	579	2	Q5BD66_EMENI	Q5bd66 aspergillus
715	7	0.9	500	2	Q6X1A2_BPR03	Q6x1a2 bacterioph	788	7	0.9	580	2	Q89YL8_BACTN	Q89yl8 bacteroides
716	7	0.9	501	2	Q6X1A3_BPT6	Q6x1a3 bacterioph	789	7	0.9	581	2	Q6TB07_9PAST	Q6tb07 manheimia
717	7	0.9	502	1	DNAA_MYCLE	P46388 mycobacteri	790	7	0.9	583	1	ARSA2_FCI01	P52145 escherichia
718	7	0.9	502	2	Q5Q3F0_9CAUD	Q5qb0 enterobacte	791	7	0.9	583	1	ARSA2_FCI01	P50593 acidiophilu
719	7	0.9	503	2	Q8MQF7_CABEL	Q8mqf7 caenorhabdi	792	7	0.9	583	2	Q798A6_9Z2ZZ	Q798a6 incn plasmi
720	7	0.9	503	2	Q8EK00_SHEON	Q8ek00 shewanella	793	7	0.9	584	2	Q9NWT1_RH1LO	Q9nwt1 rhizobium l
721	7	0.9	505	2	Q5WNC5_CABER	Q5wnc5 caenorhabdi	794	7	0.9	585	2	Q9KJ13_KLEBO	Q9kj13 klebsiella
722	7	0.9	506	2	Q17537_CABEL	Q17537 caenorhabdi	795	7	0.9	586	2	Q59FG5_HUMAN	Q59fg5 homo sapien
723	7	0.9	507	2	Q6CB84_YARLI	Q6cb84 yarrowia li	796	7	0.9	587	1	RGPI_HUMAN	P46060 homo sapien
724	7	0.9	508	2	Q90790_CABEL	P90790 caenorhabdi	797	7	0.9	588	2	Q6L1L2_PICTO	Q6l1l2 picophilus
725	7	0.9	509	2	Q9VBP7_DROME	Q9vbp7 drosophila	798	7	0.9	589	1	RGPI_MOUSE	P46061 mus musculu
726	7	0.9	509	2	Q8D0L7_YERPE	Q8d0l7 yersinia pe	799	7	0.9	589	2	Q53M56_ORYSA	Q53m56 oryza sativ
727	7	0.9	510	2	Q7QKE9_ANOGA	Q7qke9 anopheles g	800	7	0.9	589	2	Q91YS2_MOUSE	Q91ys2 mus musculu
728	7	0.9	510	2	Q5FUI9_GLUOX	Q5fui9 gluconobact	801	7	0.9	589	2	Q8C2E3_MOUSE	Q8c2e3 mus musculu
729	7	0.9	512	2	Q5AQP6_EMENI	Q5aqp6 aspergillus	802	7	0.9	589	2	Q7TWM1_MOUSE	Q7twm1 mus musculu
730	7	0.9	514	2	Q9DF59_BRARE	Q9df59 brachydanio	803	7	0.9	589	2	Q6NZB5_MOUSE	Q6nzb5 mus musculu
731	7	0.9	515	1	PVRI_MOUSE	Q9jkf6 mus musculu	804	7	0.9	590	2	Q5FL18_LACAC	Q5fli8 lactobacill
732	7	0.9	515	1	PVRI_PIG	Q9gl76 sus scrofa	805	7	0.9	592	2	Q5R4P2_PONPY	Q5r4p2 pongo pygma
733	7	0.9	515	2	Q97V93_SULSO	Q97v93 sulfolobus	806	7	0.9	594	2	Q8G6K0_DICDI	Q8g6jk0 dictyosteli
734	7	0.9	516	2	Q6P9M9_MOUSE	Q6p9m9 mus musculu	807	7	0.9	596	2	Q6X194_9CAUD	Q6x194 bacterioph
735	7	0.9	516	2	Q7MOB5_VIBVY	Q7mqb5 vibrio vuln	808	7	0.9	596	2	Q6X197_BPR32	Q6x197 bacterioph
736	7	0.9	517	1	PVRI_HUMAN	Q15223 homo sapien	809	7	0.9	596	2	Q6X198_BPR27	Q6x198 bacterioph
737	7	0.9	518	1	CDC63_HALSA	Q9hms3 halobacteri	810	7	0.9	596	2	Q6X199_9CAUD	Q6x199 bacterioph
738	7	0.9	518	2	Q747N5_GEOSL	Q747n5 geobacter s	811	7	0.9	596	2	Q6X1A0_9CAUD	Q6x1a0 bacterioph
739	7	0.9	519	2	Q7S8P0_NEUCR	Q7s8p0 neurospora	812	7	0.9	596	2	Q6X1A4_9CAUD	Q6x1a4 bacterioph
740	7	0.9	524	1	CDC64_HALMA	Q5uz24 halocaula	813	7	0.9	596	2	Q6TB11_9PAST	Q6tb11 manheimia
741	7	0.9	524	2	Q5CE67_CRYHO	Q5ce67 cryptospori	814	7	0.9	596	2	Q4S436_TETNG	Q4s436 tetraodon n
742	7	0.9	526	1	KIC10_BOVIN	P06394 bos taurus	815	7	0.9	597	2	Q4PA83_USTMA	Q4pa83 ustilago ma
743	7	0.9	526	2	Q8RME3_ALCEU	Q8rm3 alcaligenes	816	7	0.9	603	2	Q5L5D2_CHLAB	Q5l5d2 chlamydomoc
744	7	0.9	527	2	Q4LSI3_9BURK	Q4ls13 burkholderi	817	7	0.9	603	2	Q5FQZ2_GLUOX	Q5fqz2 gluconobact
745	7	0.9	527	2	Q63A80_BACCC	Q63a80 bacillus ce	818	7	0.9	604	2	Q04098_ARATH	Q04098 arabidopsis
746	7	0.9	527	2	Q6HMH4_BACHK	Q6hnm4 bacillus th	819	7	0.9	605	1	NRDD_BPT4	P07071 bacterioph
747	7	0.9	529	2	Q9FDI3_9MICO	Q9fdi3 brevivacter	820	7	0.9	605	2	Q6BP07_DEBHA	Q6bp07 debaryomyce
748	7	0.9	532	2	Q7NYE6_CHRVO	Q7nye6 chromobacte	821	7	0.9	605	2	Q7V558_BPR69	Q7v558 bacterioph
749	7	0.9	536	2	Q4P008_USTMA	Q4p008 ustilago ma	822	7	0.9	610	2	Q8W6J7_9CAUD	Q8w6j7 einorhizobi
750	7	0.9	537	1	G6PI_PARUV	Q6md44 parachlamyd	823	7	0.9	610	2	Q63STV_BURPS	Q63st4 burkholderi
751	7	0.9	537	1	YDU2_SCHPO	Q13863 schizosacch	824	7	0.9	610	2	Q62J44_BURMA	Q62j44 burkholderi
752	7	0.9	537	2	Q8Q934_9CORA	Q8qq34 avian infec	825	7	0.9	612	2	Q9IZF4_9LUTE	Q9izf4 cereal yell
753	7	0.9	541	2	Q4W0D6_ASPFU	Q4wq66 aspergillus	826	7	0.9	614	2	Q4M0L8_9BURK	Q4m0l8 burkholderi
754	7	0.9	541	2	Q5B014_EMENI	Q5b014 aspergillus	827	7	0.9	616	1	GLMS_ERPE	Q9ycg6 a glucosami
755	7	0.9	543	2	Q6D418_ERWCT	Q6d418 erwinia car	828	7	0.9	617	2	Q5YU10_NOCFA	Q5yu10 nocardia fa
756	7	0.9	545	2	Q7QY12_GIALA	Q7qy12 giardia lam	829	7	0.9	619	1	CALX_CAEEL	P34452 caenorhabdi
757	7	0.9	545	2	Q6NJCS_CORDI	Q6njcs corynebacte	830	7	0.9	620	1	ORC2_YEAST	P32833 saccharomyc
758	7	0.9	545	2	Q8ZE13_YERPE	Q8ze13 yersinia ps	831	7	0.9	622	2	Q5ZIM1_CHICK	Q5zim1 gallus gall
759	7	0.9	545	2	Q66A41_YERPS	Q66a41 yersinia ps	832	7	0.9	623	2	Q96J72_HUMAN	Q96j72 homo sapien
760	7	0.9	546	2	Q5E722_VIBFL	Q5e722 vibrio fisc	833	7	0.9	623	2	Q61J15_CABER	Q61j15 caenorhabdi
761	7	0.9	546	2	Q4NZX2_9DELT	Q4nqx2 anaeromyxob	834	7	0.9	623	2	Q8YQB8_ANASP	Q8yqb8 anabaena sp

835	7	0.9	626	2	Q55N18_BACLD	Q65n18 bacillus li	908	2	Q6FSW0_CANGA	Q6fsw0 candida gla
836	7	0.9	628	2	Q82H05_STRAW	Q82h05 streptomyce	909	2	Q5H419_XANOR	Q5h419 xanthomonas
837	7	0.9	631	2	Q51X06_MAGGR	Q51xm6 magnaporthe	910	2	Q5H6E3_XANOR	Q5h6e3 xanthomonas
838	7	0.9	632	1	HIP14_HUMAN	Q8iuh5 homo sapien	911	2	Q9H2G6_HUMAN	Q9h2g6 homo sapien
839	7	0.9	632	1	HIP14_HUMAN	Q80tn5 mus musculus	912	2	Q64Z23_BACTERIDES	Q64z23 bacteroides
840	7	0.9	632	1	HIP14_HUMAN	Q7u778 synechococc	913	2	Q55BF3_DICTDI	Q55bf3 dictyosteli
841	7	0.9	632	2	Q5DMW3_ARATH	Q5dmw3 arabidopsis	914	2	Q81298_ARATH	Q81298 arabidopsis
842	7	0.9	634	2	Q4PA26_USTMA	Q4paz6 ustilago ma	915	2	Q5FGI9_EHRRG	Q5fgi9 ehrlichia r
843	7	0.9	641	2	Q9KWU1_PSPHN	Q9kwu1 spingomonas	916	2	Q5HA55_EHRRG	Q5ha55 ehrlichia r
844	7	0.9	645	2	Q5NT68_THITH	Q5nt68 thibacillus	917	2	Q4IAW2_GIBZE	Q4iaw2 gibberella
845	7	0.9	646	2	Q6ZPH4_MOUSE	Q6zph4 mus musculus	918	2	Q33541_9GAMM	Q33541 endosymbion
846	7	0.9	647	2	Q73NK7_TREDE	Q73nk7 treponema d	919	2	Q6FMN9_CANGA	Q6fmn9 candida gla
847	7	0.9	649	1	LONH_METJA	Q58n12 methanococ	920	2	Q5GTM8_WOLTR	Q5gtm8 wolbachia s
848	7	0.9	649	2	Q4PIE1_USTMA	Q4piel ustilago ma	921	2	Q73G77_WOLPE	Q73g77 wolbachia p
849	7	0.9	651	2	Q6TKP9_HUMAN	Q6tkp9 homo sapien	922	2	Q4IA49_GIBZE	Q4ia49 gibberella
850	7	0.9	651	2	Q4Q848_LEIMA	Q4q848 leishmania	923	2	Q87E11_XYLFT	Q87e11 xyella fas
851	7	0.9	654	2	Q62L07_BURMA	Q62l07 burkholderi	924	2	Q9PEI2_XYLFT	Q9pei2 xyella fas
852	7	0.9	656	2	Q9SLA7_ARATH	Q9slaw arabidopsis	925	2	Q86L03_DICTDI	Q86l03 dictyosteli
853	7	0.9	659	2	Q6L1S1_PHOPR	Q6l1s1 photobacter	926	2	Q8PML3_XANAC	Q8pm13 xanthomonas
854	7	0.9	661	2	Q4V584_DROME	Q4v584 drosophila	927	2	Q4IMT3_GIBZE	Q4imt3 gibberella
855	7	0.9	661	2	Q8D582_VIBVU	Q8d582 vibrio vuln	928	2	Q4ZPU7_PSESV	Q4zpu7 pseudomonas
856	7	0.9	661	2	Q7MC29_VIBVU	Q7mc29 vibrio vuln	929	2	Q4ZKS0_PSESV	Q4zks0 pseudomonas
857	7	0.9	662	2	Q6XBJ0_MYCRH	Q6xbj0 mycobacteri	930	2	Q5NEP7_ERATY	Q5nep7 francisella
858	7	0.9	663	2	Q6BNAB_DEBHA	Q6bna8 debaryomyce	931	2	Q609K8_METCA	Q609k8 methylococc
859	7	0.9	663	2	Q67ZT9_ARATH	Q67zt9 arabidopsis	932	2	Q4UYV7_XANCP	Q4uyv7 xanthomonas
860	7	0.9	663	2	Q8RWP2_ARATH	Q8rwp2 arabidopsis	933	2	Q8P569_XANCP	Q8p569 xanthomonas
861	7	0.9	663	2	Q940B9_ARATH	Q940b9 arabidopsis	934	2	Q8P6N5_PSESM	Q8ppn2 xanthomonas
862	7	0.9	663	2	Q56ZA8_ARATH	Q56za8 arabidopsis	935	2	Q8PPN2_XANAC	Q8ppn2 xanthomonas
863	7	0.9	663	2	Q5LQA7_SILPO	Q5lqa7 silicibacte	936	2	Q9HXY4_PSEAE	Q9hxy4 pseudomonas
864	7	0.9	665	1	MTWR1_HUMAN	Q13613 homo sapien	937	2	Y231_BUCAP	Q8k985 buchnera ap
865	7	0.9	666	2	Q9KKR7_VIBCH	Q9kkrt7 vibrio chol	938	2	Q4FR11_9GAMM	Q4fr11 psychrobact
866	7	0.9	666	2	Q9SDT9_BRAJA	Q9sdt9 bradyrhizob	939	2	Q94HV9_ARATH	Q94hv9 arabidopsis
867	7	0.9	674	2	Q4N615_THEPA	Q4n615 theileria p	940	2	Q8BIB8_MOUSE	Q8bib8 mus musculu
868	7	0.9	680	2	Q8IMS5_DROME	Q8ims5 drosophila	941	2	Q4P319_USTMA	Q4p319 ustilago ma
869	7	0.9	682	2	Q5NPE2_ZYMMO	Q5npe2 zymomonas m	942	2	Q53F43_HUMAN	Q53f43 homo sapien
870	7	0.9	683	2	Q5SQ14_CANAL	Q5sq14 candida alb	943	2	Q96J83_HUMAN	Q96j83 homo sapien
871	7	0.9	684	2	Q75840_NEUCR	Q75840 neurospora	944	2	Q96J83_HUMAN	Q96j83 homo sapien
872	7	0.9	684	2	Q7X7M2_ORYSA	Q7x7m2 oryza sativ	945	2	Q6K7R9_ORYSA	Q6k7r9 oryza sativ
873	7	0.9	685	2	Q6S001_DICTDI	Q6s001 dictyosteli	946	2	Q80T97_MOUSE	Q80t97 mus musculu
874	7	0.9	687	2	Q5BBE4_EMENI	Q5bbe4 aspergillus	947	2	Q57GL2_SALCH	Q57gl2 salmonella
875	7	0.9	689	2	Q4NTX8_9DELT	Q4ntx8 anaeromyxob	948	2	Q5PL56_SALPA	Q5pl56 salmonella
876	7	0.9	693	2	Q63TE4_BURPS	Q63te4 burkholderi	949	2	Q7CP94_SALTY	Q7cp94 salmonella
877	7	0.9	695	2	Q88P84_PSEPK	Q88p84 pseudomonas	950	2	Q8XF68_SALTY	Q8xf68 salmonella
878	7	0.9	697	2	Q7QNS2_GIALA	Q7qns2 giardia lam	951	2	RNR_ECOLI	Q8xf68 salmonella
879	7	0.9	697	2	Q9VEP8_DROME	Q9vep8 drosophila	952	2	Q5H1E9_XANOR	Q5h1e9 xanthomonas
880	7	0.9	699	2	Q82E12_STRAW	Q82e12 streptomyce	953	2	Q4USQ2_XANCP	Q4usq2 xanthomonas
881	7	0.9	701	2	Q4RK98_TETNG	Q4rk98 tetraodon n	954	2	Q8NM59_CORGL	Q8nm59 corynebacte
882	7	0.9	702	2	Q8G6C8_BIFLO	Q8g6c8 bifidobacte	955	2	Q8PAW1_XANCP	Q8paw1 xanthomonas
883	7	0.9	702	2	Q4S767_TETNG	Q4s767 tetraodon n	956	2	Q69D85_ORYSA	Q69d85 oryza sativ
884	7	0.9	707	2	Q5P5D4_AZOSE	Q5p5d4 azoarcus ap	957	2	Q7PMI8_ANOGA	Q7pmi8 anopheles g
885	7	0.9	711	2	Q5BGX0_EMENI	Q5bgx0 aspergillus	958	2	Q6H6R9_ORYSA	Q6h6r9 oryza sativ
886	7	0.9	712	2	Q52KF5_MOUSE	Q52kf5 mus musculu	959	2	Q8S7P3_ARATH	Q8s7p3 arabidopsis
887	7	0.9	713	2	Q5AVY0_EMENI	Q5avy0 aspergillus	960	2	Q55CM6_DICTDI	Q55cm6 dictyosteli
888	7	0.9	717	2	Q9VAY0_DROME	Q9vay0 drosophila	961	2	Q55CM6_DICTDI	Q55cm6 dictyosteli
889	7	0.9	718	2	Q7RPJ6_PLAYO	Q7rpj6 plasmodium	962	2	Q8XDL9_ECO57	Q8xdl9 escherichia
890	7	0.9	720	2	Q5IND5_MAGGR	Q5ind5 magnaporthe	963	2	Q8XDL9_ECO57	Q8xdl9 escherichia
891	7	0.9	721	2	Q52B74_MAGGR	Q52b74 magnaporthe	964	2	Q7Q8G8_ANOGA	Q7q8g8 anopheles g
892	7	0.9	728	1	DGK1_ARATH	Q93017 arabidopsis	965	2	Q7QNU7_GIALA	Q7qnu7 giardia lam
893	7	0.9	728	2	Q9VQY0_9HERP	Q9vyqy0 ranid herpe	966	2	Q5BET9_EMENI	Q5bet9 aspergillus
894	7	0.9	730	2	Q4WXK8_ASPFU	Q4wxk8 aspergillus	967	2	Q7NMS8_GLOVI	Q7nms8 gloeobacter
895	7	0.9	733	2	Q9UBZ1_HUMAN	Q9ubz1 homo sapien	968	2	Q7NMS8_GLOVI	Q7nms8 gloeobacter
896	7	0.9	733	2	Q5QA92_XANCV	Q5qa92 xanthomonas	969	2	Q5L118_BACFN	Q5l118 bacteroides
897	7	0.9	734	2	Q7NP49_GLOVI	Q7np49 xanthomonas	970	2	Q6VAL8_9RHIZ	Q6val8 arsenite-ox
898	7	0.9	734	2	Q7NP49_GLOVI	Q4zlp5 pseudomonas	971	2	Q4T947_TETNG	Q4t947 tetraodon n
899	7	0.9	741	2	Q8ZLP5_PSESV	Q8zlp5 pseudomonas	972	2	Q6DB45_ERWCT	Q6db45 erwinia car
900	7	0.9	741	2	Q8TUF7_PSESM	Q8tuf7 pseudomonas	973	2	Q8FC25_ECOL6	Q8fc25 escherichia
901	7	0.9	745	1	HGL2_ARATH	Q87uf7 pseudomonas	974	2	Q97KM5_CLOAB	Q97km5 clostridium
902	7	0.9	745	2	Q5AB99_CANAL	P46607 arabidopsis	975	2	Q8PC35_ECOL6	Q8pc35 escherichia
903	7	0.9	747	2	Q9CSF1_ARATH	Q9csf1 candida alb	976	2	Q97KM5_CLOAB	Q97km5 clostridium
904	7	0.9	747	2	Q7P2X4_FUSNV	Q7p2x4 fusobacteri	977	2	Q6AJ08_DSSPS	Q6aj08 desulfotale
905	7	0.9	750	2	Q8PHI0_XANAC	Q8phi0 xanthomonas	978	2	Q5KN79_CRYNE	Q5kn79 cryptococcu
906	7	0.9	755	2	Q6K624_ORYSA	Q6k624 oryza sativ	979	2	Q55YWI_CRYNE	Q55yw1 cryptococcu
907	7	0.9	756	2	Q751Y0_ASHGO	Q751y0 ashbya gos	980	2	Q6UDK3_9HERP	Q6udk3 psittacid h

```

981 7 0.9 876 2 04XV48 PLACH
982 7 0.9 876 2 05TL13 STRMU
983 7 0.9 876 2 04H729 DEIO
984 7 0.9 883 2 06CRS9 KLUIA
985 7 0.9 885 2 08AJE1 BACTN
986 7 0.9 887 2 08XV49 RALSO
987 7 0.9 888 2 09L062 ARATH
988 7 0.9 889 2 05ILM3 MAIZE
989 7 0.9 893 2 06C3K8 YARLI
990 7 0.9 897 2 07KN84 DROME
991 7 0.9 897 2 09ULK2 DROME
992 7 0.9 897 2 09VZ26 DROME
993 7 0.9 899 2 05I411 NEIME
994 7 0.9 900 2 05IM51 MAGGR
995 7 0.9 916 2 09W354 DROME
996 7 0.9 916 2 05I410 NEIME
997 7 0.9 916 2 04SN22 TETNG
998 7 0.9 918 2 04VU88 THALASIOSI
999 7 0.9 918 2 04VU87 STREA
1000 7 0.9 921 2 05ZXL2 LEGPH

O4XV48 plasmodium
Q5tl13 streptococc
Q4h729 deinococcus
Q6crs9 kluyveromyc
Q8aje1 bacteroides
Q8xv49 ralistonia s
Q9lq62 arabidopsis
Q5yim3 zea mays (m
Q6c3k8 yarrowia li
Q7kn84 drosophila
Q9ulk2 drosophila
Q9vz26 drosophila
Q5i411 neisseria m
Q5im51 magnaporthe
Q9w354 drosophila
Q5i410 neisseria m
Q4sn22 tetraodon n
Q4vu88 thalassiosi
Q4vu87 thalassiosi
Q5zxl2 legionella

ALIGNMENTS

RESULT 1
O30912 NEIME PRELIMINARY; PRT; 797 AA.
ID O30912 NEIME PRELIMINARY; PRT; 797 AA.
AC O30912;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane protein Omp85.
GN Name=Omp85;
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HH;
RX MEDLINE=98379445; PubMed=9705245; DOI=10.1006/mpat.1998.0206;
RA Manning D.S., Reschke D.K., Judd R.C.;
RT "Omp85 proteins of Neisseria gonorrhoeae and Neisseria meningitidis are similar to Haemophilus influenzae D-15-Ag and Pasteurella multocida Oma87.";
RL Microb. Pathog. 25:11-21(1998).
DR EMBL; AF021245; AAC17599.1; -; Genomic_DNA.
DR GO; GO:0019867; C:outer membrane; IEA.
DR InterPro; IPR000184; Bac_surfAg_D15.
DR InterPro; IPR010827; Surf_Ag_VNR.
DR Pfam; PF01103; Bac_surface_Ag; 1.
DR Pfam; PF07244; Surf_Ag_VNR; 5.
SQ SEQUENCE 797 AA; -88539 MW; CF911B5F70B999CF CRC64;

Query Match 100.0%; Score 797; DB 2; Length 797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLQIASALMLGIGISPLAFADFTIQDIRVEGLQRTPESTVFNVLPVKVGDTYNDTHGSA 60
Db 1 MKLQIASALMLGIGISPLAFADFTIQDIRVEGLQRTPESTVFNVLPVKVGDTYNDTHGSA 60
Qy 61 IIKSLYATGFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLSEFLAQ 120
Db 61 IIKSLYATGFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLSEFLAQ 120
Qy 121 SQYFNQATLNOAVAGLKEEYLGKGLNIQITPKVTKLARNRVIDITIDEGKSAKITDIE 180
Db 121 SQYFNQATLNOAVAGLKEEYLGKGLNIQITPKVTKLARNRVIDITIDEGKSAKITDIE 180
Qy 181 FEGNOVYSDRKLQMSLTGEGGIWTLTRSNQFNQKFAQDMKQVDFYQNNGYPDFRIL 240

```

```

181 FEGNOVYSDRKLQMSLTGEGGIWTLTRSNQFNQKFAQDMKQVDFYQNNGYPDFRIL 240
Qy 241 DTIDIQTNEKTKQTITITVHEGGRFRWGVKSTEGDTNEVPKAELEKLLTMKFGKMYEROQ 300
Db 241 DTIDIQTNEKTKQTITITVHEGGRFRWGVKSTEGDTNEVPKAELEKLLTMKFGKMYEROQ 300
Qy 301 MTAVLGEIQNRMGSGAGYSEISVQPLNPAETKTVDVFLVHIEPGRKIYVNEIHTGNNT 360
Db 301 MTAVLGEIQNRMGSGAGYSEISVQPLNPAETKTVDVFLVHIEPGRKIYVNEIHTGNNT 360
Qy 361 RDEVVRRELQRMESAPYDTSKLQSKERVELLGYFDNVQFQDAVPLAGTDPKVDLNMSLTE 420
Db 361 RDEVVRRELQRMESAPYDTSKLQSKERVELLGYFDNVQFQDAVPLAGTDPKVDLNMSLTE 420
Qy 421 RSTGSLDLISAGVWQDTGLVMSAGVSDNLFGTGKSAALRASRSKTTNLGSLSFTDPYFTA 480
Db 421 RSTGSLDLISAGVWQDTGLVMSAGVSDNLFGTGKSAALRASRSKTTNLGSLSFTDPYFTA 480
Qy 481 DGVSLGYDVGKAFDPKPKASTSIKQYKTTTACAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
Db 481 DGVSLGYDVGKAFDPKPKASTSIKQYKTTTACAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
Qy 541 YNKAPKHVADFIKKYKTKDGTGDSFGKMLYKGTVGWRNKTDTSALMPTRGYLTGVNAEIA 600
Db 541 YNKAPKHVADFIKKYKTKDGTGDSFGKMLYKGTVGWRNKTDTSALMPTRGYLTGVNAEIA 600
Qy 601 LPGSKLQYYSAATHNQTFPPPLSKTFTMLGGVEGVIAGGYGRTEIPFFPNFYGGGLGSVR 660
Db 601 LPGSKLQYYSAATHNQTFPPPLSKTFTMLGGVEGVIAGGYGRTEIPFFPNFYGGGLGSVR 660
Qy 661 GYESGTLGPKVYDEYGEKISYGNKANKVSAELLFPMGAKDARTVRLSLFADAGSVWDG 720
Db 661 GYESGTLGPKVYDEYGEKISYGNKANKVSAELLFPMGAKDARTVRLSLFADAGSVWDG 720
Qy 721 KTYDDNSSSATGGRVQNIYAGNTHKSTFTNELRYSGAGVATWLSPLGPMKFRYAYPLKK 780
Db 721 KTYDDNSSSATGGRVQNIYAGNTHKSTFTNELRYSGAGVATWLSPLGPMKFRYAYPLKK 780
Qy 781 KPDEIQRFQFQLGTTTF 797
Db 781 KPDEIQRFQFQLGTTTF 797

RESULT 2
Q9UXJ31_NEIMA PRELIMINARY; PRT; 797 AA.
ID Q9UXJ31_NEIMA PRELIMINARY; PRT; 797 AA.
AC Q9UXJ31;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane protein Omp85.
GN Name=omp85; OrderedLocuNames=NMA0085;
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Z2491 / Serogroup A / Serotype 4A;
RX MEDLINE=20222556; PubMed=10761919; DOI=10.1038/35006655;
RA Parhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Felwell T., Hamlin N., Holroyd S.,
RA Jagels K., Leather S., Moule S., Mungall K.L., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Bartell B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.";
RL Nature 404:502-506(2000).
DR EMBL; AL162752; CAB83401.1; -; Genomic_DNA.
DR PIR; D82000; D82000.
DR GO; GO:0019867; C:outer membrane; IEA.
DR InterPro; IPR000184; Bac_surfAg_D15.

```



```
Qy 621 LSKTFTLMLGGEVCIAGYGRTRKEIPFFENFYGGGLSVRGYSGLTGPKVYDEYGEKIS 680
Db 621 LSKTFTLMLGGEVCIAGYGRTRKEIPFFENFYGGGLSVRGYSGLTGPKVYDEYGEKIS 680
Qy 681 YGGNKKANVAEELLFPMGAKDARTVRLSLFADAGSVWDGKTYDDNSSSSATGGRVONIYG 740
Db 681 YGGNKKANVAEELLFPMGAKDARTVRLSLFADAGSVWDGKTYDDNSSSSATGGRVONIYG 740
Qy 741 AGNTHKSTFTNELRYSAGGAVTWLSPGLPMKF 772
Db 741 AGNTHKSTFTNELRYSAGGAVTWLSPGLPMKF 772

RESULT 4
Q5F5W8_NEIG1
ID Q5F5W8_NEIG1 PRELIMINARY; PRT; 792 AA.
AC Q5F5W8;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Hypothetical protein.
GN OrderedLocusNames=NGO1801;
OS Neisseria gonorrhoeae (strain ATCC 700825 / FA 1090).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=242231;
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Lewis L.A., Gillaspay A.F., McLaughlin R.E., Gipson M., Ducey T.F.,
RA Ombey T., Hartman K., Nydick C., Carson M.B., Vaughn J., Thomson C.,
RA Song L., Lin S., Yuan X., Najaf F., Zhan M., Ren Q., Zhu H., Qi S.,
RA Kenton S.M., Lai H., White J.D., Clifton S., Roe B.A., Dyer D.W.;
RT "The complete genome sequence of Neisseria gonorrhoeae."
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE004969; AAW90419.1 -; Genomic_DNA.
DR InterPro; IPR00184; Bac_surfAg_D15.
DR InterPro; IPR010827; Surf_Ag_VNR.
DR Pfam; PF01103; Bac_surface_Ag; 1.
DR Pfam; PF07244; Surf_Ag_VNR; 5.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 792 AA; 87942 MW; 8EB06CA369C15812 CRC64;

Query Match 26.3%; Score 210; DB 2; Length 792;
Best Local Similarity 100.0%; Pred. No. 9.2e-211;
Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLKOIASALMWLGISPLAFADFTIQRVEGLQRTPESTFVNYLPVKVGDYNDTHGSA 60
Db 1 MKLKOIASALMWLGISPLAFADFTIQRVEGLQRTPESTFVNYLPVKVGDYNDTHGSA 60
Qy 61 IIKSLYATGFDDVRVETADGQLLTIVERTIGSLNITGAKMLQNDIAKKNLESFGLAQ 120
Db 61 IIKSLYATGFDDVRVETADGQLLTIVERTIGSLNITGAKMLQNDIAKKNLESFGLAQ 120
Qy 121 SQYFNQATLNQAVAGLKEEYLGKGLNIQTTPKVKLARNRVIDITIDGSKAKITDIE 180
Db 121 SQYFNQATLNQAVAGLKEEYLGKGLNIQTTPKVKLARNRVIDITIDGSKAKITDIE 180
Qy 181 FEGNQVYSDRKLQRQNSLTGGIWTWLTLS 210
Db 181 FEGNQVYSDRKLQRQNSLTGGIWTWLTLS 210

RESULT 5
P95359_NEIGO
ID P95359_NEIGO PRELIMINARY; PRT; 792 AA.
AC P95359;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane protein.
GN Name=omp85;
```

```
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=FA19;
RC MEDLINE=98379445; PubMed=9705245; DOI=10.1006/mpat.1998.0206;
RX Manning D.S., Reschke D.K., Judd R.C.;
RA "Omp85 proteins of Neisseria gonorrhoeae and Neisseria meningitidis
RT are similar to Haemophilus influenzae D-15-Ag and Pasteurella
RL multocida Oms87."
RL Microb. Pathog. 25:11-21(1998).
DR EMBL; U81959; AAC17600.1 -; Genomic_DNA.
DR GO; GO:0019867; C:outer membrane; IEA.
DR InterPro; IPR000184; Bac_surfAg_D15.
DR InterPro; IPR010827; Surf_Ag_VNR.
DR Pfam; PF01103; Bac_surface_Ag; 1.
DR Pfam; PF07244; Surf_Ag_VNR; 5.
SQ SEQUENCE 792 AA; 87868 MW; 90E32D24AA0513D8 CRC64;

Query Match 19.7%; Score 157; DB 2; Length 792;
Best Local Similarity 100.0%; Pred. No. 4.7e-155;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 332 TKTVDVFLHIEFGKLYVNEIHTGNKTRDEVVRELQMESAPYDTSKLQSKERVEL 391
Db 332 TKTVDVFLHIEFGKLYVNEIHTGNKTRDEVVRELQMESAPYDTSKLQSKERVEL 391
Qy 392 LGVFDNVQDAPVPLAGTDPKVDLNSLTERSTGSLDLSAGVQDGTGLVMSAGVSQDNLFG 451
Db 392 LGVFDNVQDAPVPLAGTDPKVDLNSLTERSTGSLDLSAGVQDGTGLVMSAGVSQDNLFG 451
Qy 452 TGKSAALRASRSKTLNGLSLFTDPYFTADGVSGLYD 488
Db 452 TGKSAALRASRSKTLNGLSLFTDPYFTADGVSGLYD 488

RESULT 6
Q7NVY6_CHRVO
ID Q7NVY6_CHRVO PRELIMINARY; PRT; 771 AA.
AC Q7NVY6;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Probable outer membrane protein.
GN OrderedLocusNames=CV2204;
OS Chromobacterium violaceum.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Chromobacterium.
OX NCBI_TaxID=536;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=ATCC 12472 / DSM 30191;
RC MEDLINE=22898280; PubMed=14500782; DOI=10.1073/pnas.1832124100;
RX Vasconcelos A.T.R., de Almeida D.F., Hungria M., Guimaraes C.T.,
RA Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.,
RA Alves-Gomes J.A., Andrade E.M., Araripe J., de Araujo M.F.F.,
RA Atolfi-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,
RA Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,
RA Bordignon J., Brigido M.M., Brito C.A., Brocchi M., Burity H.A.,
RA Camargo A.A., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,
RA Carvalho C.M.B., Cascardo J.C.M., Cavada B.S., Chueire L.M.O.,
RA Creczynski-Pasa T.B., Cunha-Junior N.C., Fagundes N., Falcao C.L.,
RA Fantinatti F., Farias I.P., Felipe M.S.S., Ferrari L.P., Ferro J.A.,
RA Ferro M.I.T., Franco G.R., Freitas N.S.A., Furlan L.R.,
RA Gazzinelli R.T., Gomes E.A., Goncalves P.R., Grangeiro T.B.,
RA Grattapaglia D., Grissard E.C., Hanna E.S., Jardim S.N., Laurino J.,
RA Leoi L.C.T., Lima L.F.A., Loureiro M.F., Lyra M.C.C.P.,
RA Madeira H.M.F., Manfio G.P., Maranhao A.Q., Martins W.S.,
RA di Mauro S.M.Z., de Medeiros S.R.B., Meisner R.V., Moreira M.A.M.,
RA Nascimento F.F., Nicolas M.F., Oliveira J.G., Oliveira S.C.,
RA Paixao R.F.C., Parente J.A., Pedrosa F.O., Pena S.D.J., Pereira J.O.,
```



DB 474 DPYFTADGVSGLGY 486

RESULT 8

Q88H14\_PSEPK  
 ID Q88H14\_PSEPK PRELIMINARY; PRT; 787 AA.  
 AC Q88H14  
 DT 01-JUN-2003 (TREMBLrel. 24, Created)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Bacterial surface antigen family protein.  
 GN OrderedLocusNames=PP3373;  
 OS Pseudomonas putida (strain KT2440).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 ON NCBI\_TaxID=160488;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22423060; PubMed=12534463;  
 DOI=10.1046/j.1462-9290.2002.00366.x;  
 RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,  
 RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,  
 RA Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,  
 RA Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,  
 RA Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,  
 RA Woarheez A., Uterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,  
 RA Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,  
 RA Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,  
 RA Fraser C.M.;  
 RA "Complete genome sequence and comparative analysis of the  
 RT metabolically versatile Pseudomonas putida KT2440.";  
 RL Environ. Microbiol. 4:799-808(2002).  
 DR ENBL; AS016786; AAN68977.1; -; Genomic\_DNA.  
 DR TIGR; PP3373; -.  
 DR GO; GO:0019867; C:outer membrane; IEA.  
 DR InterPro; IPR000184; Bac surfAg D15.  
 DR InterPro; IPR010827; SurfAg VNR.  
 DR Pfam; PF01103; Bac surface\_Ag; 1.  
 DR Pfam; PF07244; SurfAg\_VNR; 5.  
 KW Complete proteome.  
 SQ SEQUENCE 787 AA; 86513 MW; 41FE04CE311A6A97 CRC64;

Query Match 1.6%; Score 13; DB 2; Length 787;  
 Best Local Similarity 100.0%; Pred. No. 0.001;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps

Qy 475 DPYFTADGVSGLGY 487  
 |||||  
 DB 474 DPYFTADGVSGLGY 486  
 |||||

RESULT 9

Q8X213\_RALSO  
 ID Q8X213\_RALSO PRELIMINARY; PRT; 765 AA.  
 AC Q8X213  
 DT 01-MAR-2002 (TREMBLrel. 20, Created)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE PUTATIVE OUTER MEMBRANE SIGNAL PEPTIDE PROTEIN.  
 GN OrderedLocusNames=RSCL412; ORFNames=RS05280;  
 OS Ralstonia solanacearum (Pseudomonas solanacearum).  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 OC Burkholderiaceae; Ralstonia.  
 ON NCBI\_TaxID=305;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STPAIN=GN11000.  
 RX MEDLINE=12618179; PubMed=11823852; DOI=10.1038/415497a;  
 RA Alanoubat M., Genin S., Arriguenave F., Gouzy J., Mangenot S.,  
 RA Arlat M., Billaut A., Brottier P., Camus J.C., Cattolico L.,  
 RA Chandler M., Choigne N., Claudel-Renard C., Cunnac S., Demange N.,  
 RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,  
 RA Siguer P., Thebaud P., Whalen M., Wincker P., Levy M..

```

RA Weissenbach J., Boucher C.A.;
RT "genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
DR EMBL; AL646064; CAD15114.1; -; Genomic_DNA.
DR GO; GO:0019867; C:outer membrane; IEA.
DR InterPro; IPR002198; ADH short.
DR InterPro; IPR000184; Bac_surfAg_D15.
DR InterPro; IPR010827; Surf_Ag_VNR.
DR Pfam; PF01103; Bac_surface_Ag; 1.
DR Pfam; PF07244; Surf_Ag_VNR; 5.
DR PROSITE; PS00061; ADH_SHORT; UNKNOWN 1.
KW Complete proteome.
SQ SEQUENCE 765 AA; 85878 MW; 378641FB9F247C68 CRC64;

Query Match 1.3%; Score 10; DB 2; Length 765;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 359 KTRDEVVRE 368
DB 365 KTRDEVVRE 374

RESULT 10
Q5NZG7_AZOSE PRELIMINARY; PRT; 766 AA.
AC Q5NZG7;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Probable outer membrane protein/surface antigen.
GN OrderedLocNames=AZOSEA34220; ORFNames=eBA5996;
OS Azocarcus sp. (strain EBN1).
OC Bacteria; Proteobacteria; Betaproteobacteria; Rhodocyclales;
OC Rhodocyclaceae; Azocarcus.
OX NCBI_TaxID=76114;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=EBN1;
RX PubMed=15551059; DOI=10.1007/s00203-004-0742-9;
RA Rabus R., Kube M., Heider J., Beck A., Heitmann K., Widdel F.,
RA Reinhardt R.;
RT "the genome sequence of an anaerobic aromatic-degrading denitrifying
RT bacterium, strain EBN1.";
RL Arch. Microbiol. 183:27-36(2005).
DR EMBL; CR555306; CAI09547.1; -; Genomic_DNA.
DR GO; GO:0019867; C:outer membrane; IEA.
DR InterPro; IPR000184; Bac_surfAg_D15.
DR InterPro; IPR010827; Surf_Ag_VNR.
DR Pfam; PF01103; Bac_surface_Ag; 1.
DR Pfam; PF07244; Surf_Ag_VNR; 5.
KW Complete proteome.
SQ SEQUENCE 766 AA; 85845 MW; 3C7AA8475E5C8CB2 CRC64;

Query Match 1.3%; Score 10; DB 2; Length 766;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 359 KTRDEVVRE 368
DB 360 KTRDEVVRE 369

RESULT 11
Q9SMN7_ARATH PRELIMINARY; PRT; 328 AA.
AC Q9SMN7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein t8p19.130.
GN Name=t8p19.130;
OS Arabidopsis thaliana (Mouse-ear cress).

```

```

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eursids 11; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Choiane N., Robert C., Brottier P., Wincker P., Cattolico L.,
RA Artiguenave F., Saurin W., Weissenbach J., Mewes H.W., Lemcke K.,
RA Mayer K.F.X., Quetier F., Salanoubat N.;
RA Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA EU Arabidopsis sequencing project;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL133315; CAB62351.1; -; Genomic_DNA.
DR PIR; T46206; T46206.
DR InterPro; IPR000184; Bac_surfAg_D15.
DR Pfam; PF01103; Bac_surface_Ag; 1.
KW Hypothetical protein.
SQ SEQUENCE 328 AA; 36233 MW; CDB4D2B1EA2530C6 CRC64;

Query Match 1.1%; Score 9; DB 2; Length 328;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 654 GGLGVRGY 662
DB 152 GGLGVRGY 160

RESULT 12
Q6L543_ORYSA PRELIMINARY; PRT; 361 AA.
ID Q6L543_ORYSA PRELIMINARY;
AC Q6L543;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein OJ1005_B11.2.
GN Names=OJ1005_B11.2;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
RA Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
RA Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,
RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
RA Wu H.-P., Shaw J.-F.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC108873; AAT44133.1; -; Genomic_DNA.
DR Gramene; Q6L543; -.
DR InterPro; IPR000184; Bac_surfAg_D15.
DR Pfam; PF01103; Bac_surface_Ag; 1.
KW Hypothetical protein.
SQ SEQUENCE 361 AA; 38699 MW; 2737C18E5F63779E CRC64;

Query Match 1.1%; Score 9; DB 2; Length 361;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 654 GGLGVRGY 662
DB 255 GGLGVRGY 263

RESULT 13
Q5PP51_ARATH PRELIMINARY; PRT; 362 AA.
ID Q5PP51_ARATH PRELIMINARY;
AC Q5PP51;

```



DT 01-FEB-2005 (TrEMBLrel. 29, Created)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Ac3944160.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN NUCLEOTIDE SEQUENCE.  
RP Kim C.J., Chen H., Cheuk R., Shinn P., Ecker J.R.;  
RA "Arabidopsis ORF clones."  
RT Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.  
RL [2]  
RN NUCLEOTIDE SEQUENCE.  
RP Kim C.J., Chen H., Cheuk R., Shinn P., Ecker J.R.;  
RA "Arabidopsis ORF clones."  
RT Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
RL EMBL; BT020246; AAU74240.1; -; mRNA.  
DR EMBL; BT021139; AAX22274.1; -; mRNA.  
DR InterPro; IPR000184; Bac\_surfAg\_D15.  
DR Pfam; PF01103; Bac\_surface\_Ag; 1.  
SQ SEQUENCE 362 AA; 39010 MW; 383B1596A41F660A CRC64;  
  
Query Match 1.1%; Score 9; DB 2; Length 362;  
Best Local Similarity 100.0%; Pred. No. 8.3;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 654 GGLGSRVGY 662  
Db 255 GGLGSRVGY 263  
|||||  
  
RESULT 14  
Q9LXP7\_ARATH PRELIMINARY; PRT; 435 AA.  
AC Q9LXP7;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein F26G5\_110.  
GN Name=F26G5\_110;  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA D'Angelo M., Vezzi A., Modesto D., Pigazzi M., Valle G., Mewes H.W.,  
RA Rudd S., Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;  
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA EU Arabidopsis sequencing project;  
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL353814; CAB88424.1; -; Genomic\_DNA.  
DR PIR; T49132; T49132.  
DR InterPro; IPR000184; Bac\_surfAg\_D15.  
DR Pfam; PF01103; Bac\_surface\_Ag; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 435 AA; 47528 MW; C148B36074E49427 CRC64;

Query Match 1.1%; Score 9; DB 2; Length 435;  
Best Local Similarity 100.0%; Pred. No. 9.8;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 654 GGLGSRVGY 662  
Db 296 GGLGSRVGY 304  
|||||

RESULT 15  
Q9ZAE1\_THETH PRELIMINARY; PRT; 713 AA.  
AC Q9ZAE1;  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Polynucleotide phosphorylase.  
GN Name=pnp;  
OS Thermus thermophilus.  
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;  
OC Thermus.  
OX NCBI\_TaxID=274;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=VK1;  
RA Srganov A.A., Garber M.B., Portier C.;  
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; Z84207; CAB06341.1; -; Genomic\_DNA.  
DR HSP; P05055; 1SRO.  
DR GO; GO:0000175; F:3'-5'-exoribonuclease activity; IEA.  
DR GO; GO:0003723; F:RNA binding; IEA.  
DR GO; GO:0006396; P:RNA processing; IEA.  
DR InterPro; IPR001247; 3-ExoRNase.  
DR InterPro; IPR004087; KH.  
DR InterPro; IPR004088; KH\_type\_1.  
DR InterPro; IPR003029; S1\_1.  
DR Pfam; PF00013; KH\_1; 1.  
DR Pfam; PF03726; PNPase; 1.  
DR Pfam; PF01138; RNase\_PH; 2.  
DR Pfam; PF03725; RNase\_PH\_C; 2.  
DR Pfam; PF00575; S1\_1.  
DR SMART; SM00322; KH; 1.  
DR SMART; SM00316; S1; 1.  
DR PROSITE; PSS00084; KH\_TYPE\_1; 1.  
DR PROSITE; PSS0126; S1; 1.  
SQ SEQUENCE 713 AA; 78192 MW; 2979859D9AC5EA82 CRC64;  
  
Query Match 1.1%; Score 9; DB 2; Length 713;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 362 DEVVRREL 370  
Db 310 DEVVRREL 318  
|||||

Search completed: April 12, 2006, 16:23:17  
Job time : 282 secs

***This Page Blank (uspto)***

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 12, 2006, 16:35:33 ; Search time 28 Seconds  
(without alignments)  
1209.426 Million cell updates/sec

Title: US-10-606-618-4  
Perfect score: 797  
Sequence: 1 MKUKQIASALMLGISPLAF.....LKKKPEDEIQRFQLGTF 797

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 217505 seqs, 42489236 residues

Word size : 1  
Total number of hits satisfying chosen parameters: 217077

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Published Applications AA New:  
1: /SIDSS/prodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
2: /SIDSS/prodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
3: /SIDSS/prodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
4: /SIDSS/prodata/2/pubpaa/ECT\_NEW\_PUB.pep.\*  
5: /SIDSS/prodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
6: /SIDSS/prodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
7: /SIDSS/prodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
8: /SIDSS/prodata/2/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	210	26.3	792	6	US-10-467-657-6026
2	210	26.3	792	6	US-10-467-657-7528
3	157	19.7	792	7	US-11-103-957-92
4	7	0.9	102	6	US-10-506-454-1658
5	7	0.9	147	7	US-11-158-655-6
6	7	0.9	157	7	US-11-087-099-3827
7	7	0.9	177	7	US-11-172-740-872
8	7	0.9	222	7	US-11-096-568A-1873
9	7	0.9	222	7	US-11-096-568A-27201
10	7	0.9	238	7	US-11-188-298-16796
11	7	0.9	241	7	US-11-096-568A-1872
12	7	0.9	241	7	US-11-096-568A-27200
13	7	0.9	286	7	US-11-079-463-6578
14	7	0.9	287	7	US-11-096-568A-18041
15	7	0.9	308	7	US-11-188-298-10985
16	7	0.9	346	7	US-11-098-686-10717
17	7	0.9	349	7	US-11-079-463-10148
18	7	0.9	352	7	US-11-051-720-1325
19	7	0.9	354	7	US-11-051-720-1324
20	7	0.9	363	7	US-11-087-099-7789
21	7	0.9	363	7	US-11-051-720-1326
22	7	0.9	364	7	US-11-188-298-7183
23	7	0.9	364	7	US-11-087-099-5056
24	7	0.9	364	7	US-11-188-298-15670
25	7	0.9	366	7	US-11-188-298-1324
					Sequence 6026, Ap
					Sequence 7528, Ap
					Sequence 92, Appl
					Sequence 1658, Ap
					Sequence 6, Appl
					Sequence 3827, Ap
					Sequence 872, App
					Sequence 1873, Ap
					Sequence 27201, Ap
					Sequence 16796, A
					Sequence 1872, Ap
					Sequence 27200, A
					Sequence 6578, Ap
					Sequence 18041, A
					Sequence 10717, A
					Sequence 10148, A
					Sequence 1325, Ap
					Sequence 1324, Ap
					Sequence 7789, Ap
					Sequence 1326, Ap
					Sequence 7183, Ap
					Sequence 5056, Ap
					Sequence 15670, A
					Sequence 1324, Ap

366	7	US-11-188-298-17268	Sequence 17268, A
377	7	US-11-124-368A-209	Sequence 209, App
377	7	US-11-124-368A-210	Sequence 210, App
384	7	US-11-087-099-6378	Sequence 6378, Ap
384	7	US-11-188-298-16869	Sequence 16869, A
398	7	US-11-188-298-12144	Sequence 12144, A
399	7	US-11-188-298-13100	Sequence 13100, A
453	7	US-11-096-568A-18040	Sequence 18040, A
462	7	US-11-096-568A-12044	Sequence 12044, A
472	7	US-11-096-568A-12043	Sequence 12043, A
472	7	US-11-096-568A-18039	Sequence 18039, A
494	7	US-11-024-959-445	Sequence 445, App
512	7	US-11-188-298-19322	Sequence 19322, A
517	7	US-11-051-720-1432	Sequence 1432, Ap
549	7	US-11-085-185-2	Sequence 2, Appli
564	7	US-11-096-568A-12042	Sequence 12042, A
564	7	US-11-188-298-1110	Sequence 1110, Ap
569	7	US-11-188-298-789	Sequence 789, App
572	6	US-10-204-639-14	Sequence 14, Appl
572	7	US-11-188-298-582	Sequence 582, App
575	7	US-11-188-298-17173	Sequence 17173, A
575	7	US-11-188-298-22207	Sequence 22207, A
639	7	US-11-188-298-13558	Sequence 13558, A
666	7	US-11-055-822-48	Sequence 48, Appl
745	7	US-11-147-109-2	Sequence 2, Appli
830	6	US-10-921-793-38	Sequence 38, Appl
830	7	US-10-931-198-38	Sequence 38, Appl
830	6	US-10-942-042-38	Sequence 38, Appl
839	7	US-11-079-463-8849	Sequence 8849, Ap
1390	7	US-11-063-343-35	Sequence 35, Appl
1449	7	US-11-052-554A-237	Sequence 237, App
1458	7	US-11-096-274-2	Sequence 2, Appli
1468	6	US-10-467-657-1088	Sequence 1088, Ap
1892	7	US-11-075-185-6	Sequence 6, Appli
2431	6	US-10-958-267-6	Sequence 6, Appli
2431	6	US-10-958-267-8	Sequence 8, Appli
2432	6	US-10-958-267-12	Sequence 12, Appl
2432	6	US-11-052-554A-90	Sequence 90, Appl
3194	7	US-11-075-185-5	Sequence 5, Appli
3655	7	US-11-075-185-4	Sequence 4, Appli
3689	7	US-11-075-185-4	Sequence 4, Appli
6893	7	US-11-205-109-14	Sequence 14, Appl
6893	7	US-11-054-515-2970	Sequence 2970, Ap
15	7	US-11-266-444-2970	Sequence 2970, Ap
15	7	US-11-119-581-76	Sequence 76, Appl
18	7	US-11-035-826-247	Sequence 247, App
31	7	US-10-516-224-5	Sequence 5, Appli
34	6	US-10-516-224-5	Sequence 5, Appli
34	6	US-11-119-249-13	Sequence 13, Appli
40	7	US-11-004-399-2597	Sequence 2597, Ap
54	7	US-11-079-463-7905	Sequence 7905, Ap
60	7	US-11-079-463-8104	Sequence 8104, Ap
60	7	US-11-079-463-10066	Sequence 10066, A
60	7	US-11-188-298-21799	Sequence 21799, A
72	7	US-10-467-657-7058	Sequence 7058, Ap
75	6	US-10-467-657-7998	Sequence 7998, Ap
78	6	US-10-506-454-1042	Sequence 1042, Ap
78	6	US-11-079-463-8244	Sequence 8244, Ap
85	7	US-11-079-463-8244	Sequence 8244, Ap
85	7	US-11-096-568A-2211	Sequence 2211, Ap
91	7	US-10-467-657-3628	Sequence 3628, Ap
94	6	US-10-467-657-6394	Sequence 6394, Ap
94	6	US-11-096-568A-2205	Sequence 2205, Ap
95	7	US-11-096-568A-1030	Sequence 1030, Ap
95	7	US-11-079-463-7733	Sequence 7733, Ap
96	7	US-11-087-099-3171	Sequence 3171, Ap
96	7	US-11-107-096-79	Sequence 79, Appl
99	7	US-11-096-568A-2210	Sequence 2210, Ap
99	7	US-11-188-298-3758	Sequence 3758, Ap
99	7	US-11-096-568A-2479	Sequence 2479, Ap
100	7	US-11-096-568A-9403	Sequence 9403, Ap
103	7	US-10-501-035-356	Sequence 356, App
104	6	US-11-188-298-13304	Sequence 13304, A
105	7		

99	6	0.8	106	6	US-10-507-662-42	Sequence 42, Appl	172	6	0.8	175	7	US-11-087-099-4823	Sequence 4823, Ap
100	6	0.8	106	6	US-10-507-662-43	Sequence 43, Appl	173	6	0.8	175	7	US-11-087-099-9423	Sequence 9423, Ap
101	6	0.8	106	7	US-11-152-846-8	Sequence 8, Appl	174	6	0.8	179	7	US-11-096-568A-1165	Sequence 1165, Ap
102	6	0.8	106	7	US-11-152-846-10	Sequence 10, Appl	175	6	0.8	180	7	US-11-096-568A-9402	Sequence 9402, Ap
103	6	0.8	106	7	US-11-183-205-38	Sequence 38, Appl	176	6	0.8	182	7	US-11-052-554A-5	Sequence 5, Appl
104	6	0.8	106	7	US-11-250-411-98	Sequence 98, Appl	177	6	0.8	183	7	US-11-188-298-1411	Sequence 1411, A
105	6	0.8	106	7	US-11-250-411-103	Sequence 103, Appl	178	6	0.8	186	6	US-10-467-657-6312	Sequence 6312, Ap
106	6	0.8	107	7	US-11-221-900-6	Sequence 6, Appl	179	6	0.8	186	7	US-11-087-099-9087	Sequence 9087, Ap
107	6	0.8	107	7	US-11-221-900-8	Sequence 8, Appl	180	6	0.8	187	7	US-11-186-284-195	Sequence 195, App
108	6	0.8	107	7	US-11-221-900-9	Sequence 9, Appl	181	6	0.8	188	7	US-11-087-099-4563	Sequence 4563, Ap
109	6	0.8	107	7	US-11-284-260-25	Sequence 25, Appl	182	6	0.8	188	7	US-11-087-099-6041	Sequence 6041, Ap
110	6	0.8	107	7	US-11-284-260-26	Sequence 26, Appl	183	6	0.8	189	7	US-11-087-099-8115	Sequence 8115, Ap
111	6	0.8	107	7	US-11-284-260-27	Sequence 27, Appl	184	6	0.8	189	7	US-11-188-298-2510	Sequence 2510, Ap
112	6	0.8	107	7	US-11-284-260-28	Sequence 28, Appl	185	6	0.8	189	7	US-11-188-298-2510	Sequence 2510, Ap
113	6	0.8	107	7	US-11-284-260-29	Sequence 29, Appl	186	6	0.8	189	7	US-11-087-099-4780	Sequence 4780, Ap
114	6	0.8	107	7	US-11-284-261-25	Sequence 25, Appl	187	6	0.8	190	7	US-11-087-099-4780	Sequence 4780, Ap
115	6	0.8	107	7	US-11-284-261-26	Sequence 26, Appl	188	6	0.8	191	7	US-11-087-099-8028	Sequence 8028, Ap
116	6	0.8	107	7	US-11-284-261-27	Sequence 27, Appl	189	6	0.8	192	7	US-11-188-298-20652	Sequence 20652, Ap
117	6	0.8	107	7	US-11-284-261-28	Sequence 28, Appl	190	6	0.8	193	6	US-10-467-657-540	Sequence 540, App
118	6	0.8	107	7	US-11-284-261-29	Sequence 29, Appl	191	6	0.8	193	7	US-11-096-568A-24647	Sequence 24647, A
119	6	0.8	109	7	US-11-171-567-207	Sequence 207, Appl	192	6	0.8	193	7	US-11-188-298-4266	Sequence 4266, Ap
120	6	0.8	110	7	US-11-193-512-33	Sequence 33, Appl	193	6	0.8	195	7	US-11-079-463-7447	Sequence 7447, Ap
121	6	0.8	111	7	US-11-096-568A-1029	Sequence 1029, Ap	194	6	0.8	196	7	US-11-087-099-11349	Sequence 11349, A
122	6	0.8	112	6	US-10-793-626-2134	Sequence 2114, Ap	195	6	0.8	197	7	US-11-215-658-7	Sequence 7, Appl
123	6	0.8	112	6	US-11-188-298-13284	Sequence 13284, A	196	6	0.8	197	7	US-11-096-568A-20126	Sequence 20126, A
124	6	0.8	114	6	US-10-793-626-2252	Sequence 2252, Ap	197	6	0.8	198	7	US-11-186-284-101	Sequence 101, App
125	6	0.8	115	7	US-11-098-686-10642	Sequence 10642, A	198	6	0.8	198	7	US-11-051-724-54	Sequence 54, Appl
126	6	0.8	116	7	US-11-096-568A-6413	Sequence 6413, Ap	199	6	0.8	198	7	US-11-051-724-56	Sequence 56, Appl
127	6	0.8	116	7	US-11-079-463-6970	Sequence 6970, Ap	200	6	0.8	200	7	US-11-188-298-496	Sequence 496, App
128	6	0.8	117	7	US-11-087-099-8754	Sequence 8754, Ap	201	6	0.8	202	7	US-11-096-568A-11688	Sequence 11688, A
129	6	0.8	117	7	US-11-188-298-303	Sequence 303, Appl	202	6	0.8	203	7	US-11-098-686-10829	Sequence 10829, A
130	6	0.8	121	6	US-11-098-686-72	Sequence 72, Appl	203	6	0.8	203	7	US-11-188-298-8291	Sequence 8291, Ap
131	6	0.8	122	6	US-10-644-807-258	Sequence 258, App	204	6	0.8	204	6	US-10-793-626-2394	Sequence 2394, Ap
132	6	0.8	122	6	US-10-644-807-357	Sequence 357, App	205	6	0.8	204	7	US-11-052-554A-377	Sequence 377, App
133	6	0.8	126	7	US-11-096-568A-628	Sequence 628, Appl	206	6	0.8	204	7	US-11-096-568A-747	Sequence 747, App
134	6	0.8	128	7	US-11-355-775-54	Sequence 54, Appl	207	6	0.8	205	6	US-10-793-626-3020	Sequence 3020, Ap
135	6	0.8	128	7	US-11-250-411-87	Sequence 87, Appl	208	6	0.8	206	7	US-11-098-686-10732	Sequence 10732, A
136	6	0.8	128	7	US-11-250-411-92	Sequence 92, Appl	209	6	0.8	206	7	US-11-096-568A-16113	Sequence 16113, A
137	6	0.8	131	6	US-10-506-454-130	Sequence 130, Appl	210	6	0.8	206	7	US-11-096-568A-20184	Sequence 20184, A
138	6	0.8	131	7	US-11-096-568A-1028	Sequence 1028, Ap	211	6	0.8	207	7	US-11-096-568A-3970	Sequence 3970, Ap
139	6	0.8	134	7	US-11-072-512-2098	Sequence 2098, Ap	212	6	0.8	207	7	US-11-096-568A-9401	Sequence 9401, Ap
140	6	0.8	135	7	US-11-096-568A-23609	Sequence 23609, A	213	6	0.8	207	7	US-11-096-568A-9404	Sequence 9404, Ap
141	6	0.8	137	7	US-11-079-463-9914	Sequence 9914, Ap	214	6	0.8	208	7	US-11-129-104-97	Sequence 97, Appl
142	6	0.8	138	7	US-11-128-900-79	Sequence 79, Appl	215	6	0.8	210	7	US-11-188-298-13771	Sequence 13771, A
143	6	0.8	141	7	US-11-087-099-7283	Sequence 7283, Ap	216	6	0.8	210	7	US-11-188-298-15851	Sequence 15851, A
144	6	0.8	143	7	US-11-087-099-9821	Sequence 9821, Ap	217	6	0.8	211	7	US-11-098-686-11200	Sequence 11200, A
145	6	0.8	143	7	US-11-096-568A-1166	Sequence 1166, Ap	218	6	0.8	213	7	US-11-102-621-135	Sequence 135, App
146	6	0.8	144	7	US-11-072-512-3457	Sequence 3457, Ap	219	6	0.8	215	7	US-11-188-298-22562	Sequence 22562, A
147	6	0.8	144	7	US-11-096-568A-12215	Sequence 12215, A	220	6	0.8	216	7	US-11-087-099-13335	Sequence 12335, A
148	6	0.8	144	7	US-11-096-568A-23608	Sequence 23608, A	221	6	0.8	216	7	US-11-096-568A-18899	Sequence 18899, A
149	6	0.8	146	7	US-11-087-099-8355	Sequence 8355, Ap	222	6	0.8	218	7	US-11-096-568A-13651	Sequence 13651, A
150	6	0.8	150	5	US-09-978-360A-708	Sequence 708, App	223	6	0.8	219	6	US-10-518-019A-6	Sequence 6, Appl
151	6	0.8	154	7	US-11-188-298-9339	Sequence 9339, Ap	224	6	0.8	219	7	US-11-087-099-8268	Sequence 8268, Ap
152	6	0.8	154	7	US-11-052-554A-327	Sequence 327, Appl	225	6	0.8	223	6	US-10-508-263-119	Sequence 119, App
153	6	0.8	155	7	US-11-087-099-3541	Sequence 3541, Ap	226	6	0.8	225	6	US-10-793-626-1594	Sequence 1594, Ap
154	6	0.8	155	7	US-11-096-568A-627	Sequence 627, Appl	227	6	0.8	226	7	US-11-188-298-21324	Sequence 21324, A
155	6	0.8	157	7	US-11-087-099-4136	Sequence 4136, Ap	228	6	0.8	229	7	US-11-188-298-11181	Sequence 11181, A
156	6	0.8	158	7	US-11-079-463-6106	Sequence 6106, Ap	229	6	0.8	231	7	US-11-096-568A-7771	Sequence 7771, Ap
157	6	0.8	158	7	US-11-188-298-4807	Sequence 4807, Ap	230	6	0.8	233	7	US-11-087-099-1395	Sequence 1395, Ap
158	6	0.8	159	7	US-11-087-099-5905	Sequence 5905, Ap	231	6	0.8	234	7	US-11-188-298-19658	Sequence 19658, A
159	6	0.8	159	7	US-11-051-724-58	Sequence 58, Appl	232	6	0.8	235	7	US-11-096-568A-18863	Sequence 18863, A
160	6	0.8	160	7	US-11-057-012-7	Sequence 7, Appl	233	6	0.8	235	7	US-11-284-260-5	Sequence 5, Appl
161	6	0.8	160	7	US-10-714-740-2161	Sequence 2161, Ap	234	6	0.8	235	7	US-11-087-099-11734	Sequence 11734, A
162	6	0.8	161	6	US-10-714-740-294	Sequence 294, App	235	6	0.8	236	7	US-11-096-568A-16112	Sequence 16112, A
163	6	0.8	162	7	US-11-215-658-8	Sequence 8, Appl	236	6	0.8	236	7	US-11-096-568A-27570	Sequence 27570, A
164	6	0.8	162	7	US-11-096-568A-14219	Sequence 14219, A	237	6	0.8	236	7	US-11-096-568A-29000	Sequence 29000, A
165	6	0.8	165	6	US-10-475-075-803	Sequence 803, App	238	6	0.8	236	7	US-11-096-568A-29000	Sequence 875, App
166	6	0.8	165	6	US-11-188-298-21132	Sequence 21132, A	239	6	0.8	239	7	US-11-000-463-875	Sequence 876, App
167	6	0.8	166	6	US-10-506-454-824	Sequence 824, App	240	6	0.8	239	7	US-11-000-463-875	Sequence 7433, App
168	6	0.8	167	7	US-11-096-568A-3391	Sequence 3391, Ap	241	6	0.8	239	7	US-11-096-568A-7433	Sequence 32542, A
169	6	0.8	172	7	US-11-096-568A-5913	Sequence 5913, Ap	242	6	0.8	239	7	US-11-096-568A-32542	Sequence 32542, A
170	6	0.8	172	7	US-11-096-568A-33907	Sequence 33907, A	243	6	0.8	240	7	US-11-096-568A-24894	Sequence 24894, A
171	6	0.8	173	7	US-11-079-463-6942	Sequence 6942, Ap	244	6	0.8	241	6	US-10-878-558A-35	Sequence 35, Appl

245	6	0.8	242	7	US-11-188-298-6437	Sequence 6437, Ap	318	6	0.8	264	7	US-11-096-568A-25556	Sequence 25556, A
246	6	0.8	243	6	US-10-506-454-277	Sequence 277, App	319	6	0.8	265	7	US-11-072-512-2141	Sequence 2141, Ap
247	6	0.8	243	7	US-11-096-568A-7432	Sequence 7432, Ap	320	6	0.8	266	7	US-11-098-686-10476	Sequence 10476, A
248	6	0.8	243	7	US-11-096-568A-9662	Sequence 9662, Ap	321	6	0.8	267	6	US-10-501-035-293	Sequence 293, App
249	6	0.8	243	7	US-11-096-568A-18898	Sequence 18898, A	322	6	0.8	267	6	US-10-506-454-380	Sequence 380, App
250	6	0.8	243	7	US-11-096-568A-24644	Sequence 24644, A	323	6	0.8	267	7	US-11-096-568A-9661	Sequence 9661, Ap
251	6	0.8	244	6	US-10-467-657-8278	Sequence 8278, Ap	324	6	0.8	269	7	US-11-000-463-403	Sequence 403, App
252	6	0.8	244	7	US-11-096-568A-27569	Sequence 27569, Ap	325	6	0.8	269	7	US-11-224-726-1	Sequence 1, Appli
253	6	0.8	244	7	US-11-096-568A-31975	Sequence 31975, A	326	6	0.8	271	6	US-10-467-657-7690	Sequence 7690, Ap
254	6	0.8	244	7	US-11-096-568A-31975	Sequence 31975, A	327	6	0.8	271	6	US-11-070-080-19	Sequence 19, Appl
255	6	0.8	244	7	US-11-079-463-8622	Sequence 8622, Ap	328	6	0.8	273	7	US-11-096-568A-19157	Sequence 19157, A
256	6	0.8	244	7	US-11-079-463-9308	Sequence 9308, Ap	329	6	0.8	273	7	US-11-072-512-3353	Sequence 3353, Ap
257	6	0.8	245	7	US-11-188-298-10984	Sequence 10984, A	330	6	0.8	274	6	US-10-506-454-159	Sequence 159, App
258	6	0.8	246	7	US-11-098-686-11424	Sequence 11424, A	331	6	0.8	276	7	US-11-096-568A-9660	Sequence 9660, Ap
259	6	0.8	246	7	US-11-051-720-1371	Sequence 1371, Ap	332	6	0.8	278	7	US-11-079-463-9219	Sequence 9219, Ap
260	6	0.8	246	7	US-11-096-568A-7431	Sequence 7431, Ap	333	6	0.8	280	7	US-11-079-463-7570	Sequence 7570, Ap
261	6	0.8	247	7	US-11-054-515-1384	Sequence 1384, Ap	334	6	0.8	281	7	US-11-096-568A-33368	Sequence 33368, A
262	6	0.8	247	7	US-11-266-444-1384	Sequence 1384, Ap	335	6	0.8	282	7	US-11-096-568A-15872	Sequence 15872, A
263	6	0.8	248	7	US-11-087-099-5851	Sequence 5851, Ap	336	6	0.8	282	7	US-10-506-454-1410	Sequence 1410, Ap
264	6	0.8	248	7	US-11-096-568A-3390	Sequence 3390, Ap	337	6	0.8	283	7	US-11-096-568A-13650	Sequence 13650, A
265	6	0.8	249	7	US-11-087-099-8891	Sequence 8891, Ap	338	6	0.8	283	7	US-11-096-568A-27955	Sequence 27955, A
266	6	0.8	249	7	US-11-096-568A-24893	Sequence 24893, A	339	6	0.8	284	7	US-11-096-568A-17484	Sequence 17484, A
267	6	0.8	249	7	US-11-188-298-15092	Sequence 15092, A	340	6	0.8	284	7	US-11-096-568A-31905	Sequence 31905, A
268	6	0.8	250	7	US-11-096-568A-21531	Sequence 21531, A	341	6	0.8	286	6	US-10-467-657-1254	Sequence 1254, Ap
269	6	0.8	251	7	US-11-096-568A-692	Sequence 692, App	342	6	0.8	287	7	US-11-087-099-9350	Sequence 9350, Ap
270	6	0.8	251	7	US-11-096-568A-1254	Sequence 1254, Ap	343	6	0.8	287	7	US-11-096-568A-1253	Sequence 1253, Ap
271	6	0.8	251	7	US-11-096-568A-22969	Sequence 22969, A	344	6	0.8	289	7	US-11-096-568A-9987	Sequence 9987, Ap
272	6	0.8	251	7	US-11-096-568A-30834	Sequence 30834, A	345	6	0.8	289	7	US-11-188-298-11404	Sequence 11404, A
273	6	0.8	252	7	US-11-188-298-8041	Sequence 8041, Ap	346	6	0.8	291	7	US-11-096-568A-1252	Sequence 1252, Ap
274	6	0.8	252	7	US-11-096-568A-9604	Sequence 9604, Ap	347	6	0.8	292	7	US-11-079-463-7825	Sequence 7825, Ap
275	6	0.8	252	7	US-11-188-298-2118	Sequence 2118, Ap	348	6	0.8	293	6	US-10-485-517-203	Sequence 203, App
276	6	0.8	252	7	US-11-188-298-6337	Sequence 6337, Ap	349	6	0.8	293	7	US-11-098-686-10638	Sequence 10638, A
277	6	0.8	252	7	US-11-188-298-9811	Sequence 9811, Ap	350	6	0.8	294	7	US-11-096-568A-18862	Sequence 18862, A
278	6	0.8	252	7	US-11-188-298-10101	Sequence 10101, A	351	6	0.8	294	7	US-11-096-568A-24355	Sequence 24355, A
279	6	0.8	252	7	US-11-188-298-10667	Sequence 10667, A	352	6	0.8	297	7	US-11-096-568A-16867	Sequence 16867, A
280	6	0.8	252	7	US-11-188-298-12269	Sequence 12269, A	353	6	0.8	297	7	US-11-055-822-922	Sequence 922, App
281	6	0.8	252	7	US-11-188-298-20288	Sequence 20288, A	354	6	0.8	297	6	US-11-096-568A-9603	Sequence 9603, Ap
282	6	0.8	253	7	US-11-087-099-6400	Sequence 6400, Ap	355	6	0.8	298	6	US-10-467-657-4362	Sequence 4362, Ap
283	6	0.8	253	7	US-11-188-298-7171	Sequence 7171, Ap	356	6	0.8	299	6	US-10-793-626-1192	Sequence 1192, Ap
284	6	0.8	253	7	US-11-188-298-8654	Sequence 8654, Ap	357	6	0.8	299	6	US-10-467-657-4424	Sequence 4424, Ap
285	6	0.8	253	7	US-11-188-298-10108	Sequence 10108, A	358	6	0.8	299	6	US-10-467-657-4424	Sequence 4424, Ap
286	6	0.8	253	7	US-11-188-298-12998	Sequence 12998, A	359	6	0.8	300	7	US-11-087-099-4351	Sequence 4351, Ap
287	6	0.8	253	7	US-11-188-298-21747	Sequence 21747, Ap	360	6	0.8	300	7	US-11-079-463-6102	Sequence 6102, Ap
288	6	0.8	254	7	US-11-188-298-8486	Sequence 8486, Ap	361	6	0.8	301	7	US-11-096-568A-18861	Sequence 18861, A
289	6	0.8	254	7	US-11-188-298-17044	Sequence 17044, A	362	6	0.8	301	7	US-11-096-568A-24354	Sequence 24354, A
290	6	0.8	254	7	US-11-188-298-17124	Sequence 17124, A	363	6	0.8	304	6	US-10-934-944-286	Sequence 286, App
291	6	0.8	255	7	US-11-098-686-10492	Sequence 10492, A	364	6	0.8	304	7	US-11-116-881A-295	Sequence 295, App
292	6	0.8	255	7	US-11-188-298-4721	Sequence 4721, Ap	365	6	0.8	304	7	US-11-188-298-4657	Sequence 4657, Ap
293	6	0.8	255	7	US-11-188-298-5790	Sequence 5790, Ap	366	6	0.8	305	7	US-11-096-568A-31765	Sequence 31765, A
294	6	0.8	255	7	US-11-188-298-12957	Sequence 12957, A	367	6	0.8	307	7	US-11-055-822-528	Sequence 528, App
295	6	0.8	255	7	US-11-188-298-14332	Sequence 14332, A	368	6	0.8	308	7	US-11-188-298-12821	Sequence 12821, A
296	6	0.8	255	7	US-11-188-298-16836	Sequence 16836, A	369	6	0.8	309	7	US-11-185-460-2	Sequence 2, Appli
297	6	0.8	255	7	US-11-188-298-17949	Sequence 17949, A	370	6	0.8	310	7	US-11-079-463-5549	Sequence 5549, Ap
298	6	0.8	255	7	US-11-188-298-18645	Sequence 18645, A	371	6	0.8	310	7	US-11-079-463-9722	Sequence 9722, Ap
299	6	0.8	255	7	US-11-188-298-20488	Sequence 20488, A	372	6	0.8	312	7	US-11-172-740-1772	Sequence 1772, Ap
300	6	0.8	256	6	US-10-467-657-6124	Sequence 6124, Ap	373	6	0.8	313	7	US-11-052-554A-316	Sequence 316, App
301	6	0.8	256	7	US-11-096-568A-3389	Sequence 3389, Ap	374	6	0.8	313	7	US-11-186-084-269	Sequence 269, App
302	6	0.8	256	7	US-11-096-568A-22968	Sequence 22968, A	375	6	0.8	313	7	US-11-186-084-269	Sequence 3, Appli
303	6	0.8	256	7	US-11-188-298-2484	Sequence 2484, Ap	376	6	0.8	313	7	US-11-091-936-3	Sequence 9309, Ap
304	6	0.8	258	7	US-11-079-463-6370	Sequence 6370, Ap	377	6	0.8	313	7	US-11-188-298-9309	Sequence 21335, A
305	6	0.8	259	7	US-11-096-568A-5912	Sequence 5912, Ap	378	6	0.8	313	7	US-11-188-298-21335	Sequence 9886, Ap
306	6	0.8	259	7	US-11-096-568A-28999	Sequence 28999, A	379	6	0.8	314	7	US-11-096-568A-8986	Sequence 7304, Ap
307	6	0.8	259	7	US-11-188-298-17925	Sequence 17925, A	380	6	0.8	314	7	US-11-079-463-7384	Sequence 8985, Ap
308	6	0.8	260	7	US-11-096-568A-31906	Sequence 31906, A	381	6	0.8	316	7	US-11-096-568A-8985	Sequence 8985, Ap
309	6	0.8	260	7	US-11-188-298-10818	Sequence 10818, A	382	6	0.8	316	7	US-11-096-568A-8988	Sequence 8988, Ap
310	6	0.8	261	7	US-11-000-463-404	Sequence 404, App	383	6	0.8	316	7	US-11-096-568A-21530	Sequence 21530, A
311	6	0.8	261	7	US-11-096-568A-15155	Sequence 15155, A	384	6	0.8	316	7	US-11-188-298-16788	Sequence 16788, A
312	6	0.8	261	7	US-11-096-568A-19159	Sequence 19159, A	385	6	0.8	317	6	US-10-873-528-65	Sequence 65, Appl
313	6	0.8	261	7	US-11-096-568A-22967	Sequence 22967, A	386	6	0.8	317	7	US-11-096-568A-25604	Sequence 25604, A
314	6	0.8	261	7	US-11-096-568A-25557	Sequence 25557, A	387	6	0.8	317	7	US-11-079-463-8051	Sequence 8051, Ap
315	6	0.8	263	7	US-11-188-298-18423	Sequence 18423, A	388	6	0.8	318	7	US-11-098-686-11281	Sequence 11281, A
316	6	0.8	264	7	US-11-096-568A-15154	Sequence 15154, A	389	6	0.8	318	7	US-11-087-099-12185	Sequence 12185, A
317	6	0.8	264	7	US-11-096-568A-19158	Sequence 19158, A	390	6	0.8	318	7	US-11-096-568A-8399	Sequence 8399, Ap

391	6	0.8	318	7	US-11-096-568A-23270	Sequence 23270, A	464	6	0.8	345	7	US-11-098-686-10460	Sequence 10460, A
392	6	0.8	320	6	US-10-793-626-2988	Sequence 2988, A	465	6	0.8	345	7	US-11-087-099-1292	Sequence 1292, Ap
393	6	0.8	320	6	US-10-995-561-947	Sequence 947, App	466	6	0.8	345	7	US-11-188-298-6310	Sequence 6310, Ap
394	6	0.8	320	7	US-11-087-099-3546	Sequence 3546, Ap	467	6	0.8	345	7	US-11-188-298-15246	Sequence 15246, A
395	6	0.8	320	7	US-11-096-568A-6440	Sequence 6440, A	468	6	0.8	345	7	US-11-188-298-18248	Sequence 18248, A
396	6	0.8	320	7	US-11-096-568A-25656	Sequence 25656, A	469	6	0.8	346	7	US-11-087-099-8092	Sequence 8092, Ap
397	6	0.8	322	7	US-11-079-463-5582	Sequence 5582, Ap	470	6	0.8	347	7	US-11-072-512-2844	Sequence 2844, Ap
398	6	0.8	322	7	US-11-188-298-14564	Sequence 14564, A	471	6	0.8	347	7	US-11-087-099-4236	Sequence 4236, Ap
399	6	0.8	322	7	US-11-188-298-19156	Sequence 19156, A	472	6	0.8	347	7	US-11-096-568A-746	Sequence 746, App
400	6	0.8	324	7	US-11-188-298-22535	Sequence 22535, A	473	6	0.8	347	7	US-11-188-298-3956	Sequence 3956, Ap
401	6	0.8	324	7	US-11-096-568A-23269	Sequence 23269, A	474	6	0.8	347	7	US-11-235-621-5	Sequence 5, Appl1
402	6	0.8	325	7	US-11-072-512-3320	Sequence 3320, Ap	475	6	0.8	348	7	US-11-087-099-7875	Sequence 7875, Ap
403	6	0.8	325	7	US-11-096-568A-23268	Sequence 23268, A	476	6	0.8	348	7	US-11-087-099-9659	Sequence 9659, Ap
404	6	0.8	325	7	US-11-096-568A-31764	Sequence 31764, A	477	6	0.8	348	7	US-11-096-568A-22171	Sequence 22171, A
405	6	0.8	326	7	US-11-087-099-10002	Sequence 10002, A	478	6	0.8	348	7	US-11-188-298-18304	Sequence 18304, A
406	6	0.8	327	7	US-11-096-568A-29399	Sequence 29399, A	479	6	0.8	348	7	US-11-188-298-19437	Sequence 19437, A
407	6	0.8	328	7	US-11-199-233-8	Sequence 8, Appl1	480	6	0.8	348	7	US-11-188-298-19966	Sequence 19966, A
408	6	0.8	329	7	US-11-096-568A-5471	Sequence 5471, Ap	481	6	0.8	348	7	US-11-188-298-21606	Sequence 21606, A
409	6	0.8	329	7	US-11-096-568A-7770	Sequence 7770, Ap	482	6	0.8	349	7	US-11-087-099-11115	Sequence 11115, A
410	6	0.8	329	7	US-11-188-298-13197	Sequence 13197, A	483	6	0.8	349	7	US-11-188-298-705	Sequence 705, App
411	6	0.8	331	7	US-11-079-463-5495	Sequence 5495, Ap	484	6	0.8	349	7	US-11-188-298-8323	Sequence 8323, Ap
412	6	0.8	332	7	US-11-087-099-8851	Sequence 8851, Ap	485	6	0.8	349	7	US-11-188-298-10263	Sequence 10263, A
413	6	0.8	332	7	US-11-096-568A-24353	Sequence 24353, A	486	6	0.8	349	7	US-11-188-298-13758	Sequence 13758, A
414	6	0.8	333	6	US-10-467-657-6974	Sequence 6974, Ap	487	6	0.8	350	7	US-11-096-568A-30833	Sequence 30833, A
415	6	0.8	333	7	US-11-087-099-1297	Sequence 1297, Ap	488	6	0.8	350	7	US-11-188-298-3489	Sequence 3489, Ap
416	6	0.8	333	7	US-11-087-099-6987	Sequence 6987, Ap	489	6	0.8	350	7	US-11-188-298-14066	Sequence 14066, A
417	6	0.8	333	7	US-11-087-099-7269	Sequence 7269, Ap	490	6	0.8	350	7	US-11-188-298-17678	Sequence 17678, A
418	6	0.8	333	7	US-11-087-099-7274	Sequence 7274, Ap	491	6	0.8	350	7	US-11-188-298-22365	Sequence 22365, A
419	6	0.8	333	7	US-11-096-568A-6439	Sequence 6439, Ap	492	6	0.8	351	7	US-11-087-099-8518	Sequence 8518, Ap
420	6	0.8	333	7	US-11-188-298-3343	Sequence 3343, Ap	493	6	0.8	351	7	US-11-087-099-12353	Sequence 12353, A
421	6	0.8	334	7	US-11-087-099-2916	Sequence 2916, Ap	494	6	0.8	351	7	US-11-096-568A-23008	Sequence 23008, A
422	6	0.8	334	7	US-11-087-099-9197	Sequence 9197, Ap	495	6	0.8	351	7	US-11-188-298-6905	Sequence 6905, Ap
423	6	0.8	334	7	US-11-096-568A-12234	Sequence 12234, A	496	6	0.8	352	6	US-10-467-657-984	Sequence 984, App
424	6	0.8	334	7	US-11-188-298-10242	Sequence 10242, A	497	6	0.8	352	7	US-11-087-099-6436	Sequence 6436, Ap
425	6	0.8	335	7	US-11-087-099-5159	Sequence 5159, Ap	498	6	0.8	352	7	US-11-096-568A-31974	Sequence 31974, A
426	6	0.8	336	6	US-10-194-487-182	Sequence 182, App	499	6	0.8	353	7	US-11-188-298-16925	Sequence 16925, A
427	6	0.8	336	6	US-10-195-883-182	Sequence 182, App	500	6	0.8	353	7	US-11-188-298-3584	Sequence 3584, Ap
428	6	0.8	336	6	US-10-195-888-182	Sequence 182, App	501	6	0.8	354	7	US-11-087-099-11419	Sequence 11419, A
429	6	0.8	336	6	US-10-195-889-182	Sequence 182, App	502	6	0.8	355	7	US-11-096-568A-46481	Sequence 46481, A
430	6	0.8	336	6	US-11-087-099-6779	Sequence 6779, Ap	503	6	0.8	355	7	US-11-188-298-7439	Sequence 7439, Ap
431	6	0.8	337	7	US-11-096-568A-33541	Sequence 33541, A	504	6	0.8	356	7	US-11-087-099-3068	Sequence 3068, Ap
432	6	0.8	337	7	US-11-096-568A-13649	Sequence 13649, A	505	6	0.8	356	7	US-11-087-099-12083	Sequence 12083, A
433	6	0.8	338	6	US-10-467-657-8208	Sequence 8208, Ap	506	6	0.8	357	7	US-11-188-298-20200	Sequence 20200, A
434	6	0.8	338	7	US-11-016-564-4	Sequence 4, Appl1	507	6	0.8	357	7	US-11-087-099-11474	Sequence 11474, A
435	6	0.8	338	7	US-11-096-568A-8398	Sequence 8398, Ap	508	6	0.8	357	7	US-11-087-099-12365	Sequence 12365, A
436	6	0.8	338	7	US-11-096-568A-32540	Sequence 32540, A	509	6	0.8	357	7	US-11-096-568A-11144	Sequence 11144, A
437	6	0.8	339	7	US-11-010-239-117	Sequence 117, App	510	6	0.8	358	6	US-10-467-657-1438	Sequence 1438, Ap
438	6	0.8	339	7	US-11-087-099-9109	Sequence 9109, Ap	511	6	0.8	358	6	US-10-525-674-24	Sequence 24, Appl
439	6	0.8	339	7	US-11-096-568A-31793	Sequence 31793, A	512	6	0.8	358	7	US-11-127-877-66	Sequence 66, Appl
440	6	0.8	339	7	US-11-172-740-2504	Sequence 2504, Ap	513	6	0.8	358	7	US-11-087-099-5630	Sequence 5630, Ap
441	6	0.8	339	7	US-10-515-481-3	Sequence 3, Appl1	514	6	0.8	359	7	US-11-096-568A-28150	Sequence 28150, A
442	6	0.8	341	6	US-10-515-481-6	Sequence 6, Appl1	515	6	0.8	360	6	US-10-496-647-10	Sequence 10, Appl
443	6	0.8	341	6	US-10-515-481-9	Sequence 9, Appl1	516	6	0.8	360	6	US-10-496-647-12	Sequence 12, Appl
444	6	0.8	341	6	US-10-515-481-12	Sequence 12, Appl	517	6	0.8	360	6	US-10-496-647-14	Sequence 14, Appl
445	6	0.8	341	6	US-11-087-099-1836	Sequence 1836, Ap	518	6	0.8	360	6	US-10-496-647-16	Sequence 16, Appl
446	6	0.8	341	7	US-11-087-099-4333	Sequence 4333, Ap	519	6	0.8	360	7	US-11-072-512-2211	Sequence 2211, Ap
447	6	0.8	341	7	US-11-087-099-4892	Sequence 4892, Ap	520	6	0.8	361	7	US-11-087-099-2801	Sequence 2801, Ap
448	6	0.8	341	7	US-11-087-099-4892	Sequence 4892, Ap	521	6	0.8	361	7	US-11-096-568A-31792	Sequence 31792, A
449	6	0.8	341	7	US-11-087-099-7320	Sequence 7320, Ap	522	6	0.8	362	7	US-11-087-099-5211	Sequence 5211, Ap
450	6	0.8	341	7	US-11-096-568A-9986	Sequence 9986, Ap	523	6	0.8	362	7	US-11-087-099-6033	Sequence 6033, Ap
451	6	0.8	342	7	US-11-096-568A-15153	Sequence 15153, A	524	6	0.8	362	7	US-11-087-099-9090	Sequence 9090, Ap
452	6	0.8	343	7	US-11-016-564-17	Sequence 17, Appl	525	6	0.8	362	7	US-11-096-568A-6377	Sequence 6377, Ap
453	6	0.8	343	7	US-11-072-512-3068	Sequence 3068, Ap	526	6	0.8	363	7	US-11-096-568A-21529	Sequence 21529, A
454	6	0.8	343	7	US-11-087-099-2134	Sequence 2134, Ap	527	6	0.8	363	6	US-10-878-556A-14	Sequence 14, Appl
455	6	0.8	343	7	US-11-188-298-3028	Sequence 3028, Ap	528	6	0.8	363	7	US-11-098-686-10750	Sequence 10750, A
456	6	0.8	343	7	US-11-188-298-9065	Sequence 9065, Ap	529	6	0.8	363	7	US-11-096-568A-9674	Sequence 9674, Ap
457	6	0.8	343	7	US-11-188-298-10427	Sequence 10427, A	530	6	0.8	364	6	US-10-506-454-1127	Sequence 1127, Ap
458	6	0.8	344	7	US-11-072-512-3358	Sequence 3358, Ap	531	6	0.8	365	7	US-11-096-568A-9673	Sequence 9673, Ap
459	6	0.8	344	7	US-11-087-099-1307	Sequence 1307, Ap	532	6	0.8	366	7	US-11-098-686-11034	Sequence 11034, A
460	6	0.8	344	7	US-11-096-568A-19478	Sequence 19478, A	533	6	0.8	366	7	US-11-087-099-2872	Sequence 2872, Ap
461	6	0.8	344	7	US-11-079-463-8052	Sequence 8052, Ap	534	6	0.8	366	7	US-11-087-099-4133	Sequence 4133, Ap
462	6	0.8	344	7	US-11-188-298-3060	Sequence 3060, Ap	535	6	0.8	366	7	US-11-087-099-4201	Sequence 4201, Ap
463	6	0.8	344	7	US-11-188-298-17164	Sequence 17164, A	536	6	0.8	366	7	US-11-087-099-7455	Sequence 7455, Ap

537	6	0.8	366	7	US-11-087-099-9353	Sequence 9353, Ap	610	384	7	US-11-096-568A-8950	Sequence 8950, Ap
538	6	0.8	366	7	US-11-087-099-12100	Sequence 12100, A	611	384	7	US-11-096-568A-13022	Sequence 13022, A
539	6	0.8	366	7	US-11-096-568A-745	Sequence 745, App	612	385	6	US-10-995-561-945	Sequence 945, App
540	6	0.8	366	7	US-11-096-568A-31973	Sequence 31973, A	613	385	6	US-10-995-561-949	Sequence 949, App
541	6	0.8	367	7	US-11-152-366-35	Sequence 35, Appl	614	385	7	US-11-087-099-7112	Sequence 7112, Ap
542	6	0.8	367	6	US-10-858-730-217	Sequence 217, App	615	385	7	US-11-096-568A-23006	Sequence 23006, A
543	6	0.8	368	6	US-10-501-035-249	Sequence 249, App	616	386	7	US-11-087-099-11460	Sequence 11460, A
544	6	0.8	368	6	US-11-087-099-936	Sequence 936, App	617	387	7	US-11-096-568A-25143	Sequence 25143, A
545	6	0.8	368	7	US-11-087-099-4522	Sequence 4522, Ap	618	387	7	US-11-188-298-3125	Sequence 3125, Ap
546	6	0.8	368	7	US-11-087-099-9713	Sequence 9713, Ap	619	387	7	US-11-235-621-15	Sequence 15, Appl
547	6	0.8	368	7	US-11-087-099-11484	Sequence 11484, A	620	388	7	US-11-096-568A-15902	Sequence 15902, A
548	6	0.8	368	7	US-11-087-099-11862	Sequence 11862, A	621	388	7	US-11-188-298-19057	Sequence 19057, A
549	6	0.8	369	7	US-11-087-099-2275	Sequence 2275, Ap	622	389	7	US-11-087-099-7218	Sequence 7218, Ap
550	6	0.8	369	7	US-11-188-298-10395	Sequence 10395, A	623	389	7	US-11-096-568A-25142	Sequence 25142, A
551	6	0.8	370	7	US-11-087-099-5213	Sequence 5213, Ap	624	390	7	US-11-188-298-21687	Sequence 21687, A
552	6	0.8	370	7	US-11-087-099-6710	Sequence 6710, Ap	625	391	7	US-11-087-099-9851	Sequence 9851, Ap
553	6	0.8	370	7	US-11-087-099-8655	Sequence 8655, Ap	626	392	6	US-10-793-626-2494	Sequence 2494, Ap
554	6	0.8	370	7	US-11-087-099-10826	Sequence 10826, A	627	392	6	US-11-188-298-4450	Sequence 4450, Ap
555	6	0.8	370	7	US-11-087-099-11201	Sequence 11201, A	628	393	7	US-11-096-568A-34047	Sequence 34047, A
556	6	0.8	370	7	US-11-096-568A-12233	Sequence 12233, A	629	394	7	US-11-087-099-6327	Sequence 6327, Ap
557	6	0.8	370	7	US-11-188-298-6124	Sequence 6124, Ap	630	394	7	US-11-188-298-18746	Sequence 18746, A
558	6	0.8	370	7	US-11-188-298-9992	Sequence 9992, Ap	631	395	6	US-09-978-360A-769	Sequence 769, App
559	6	0.8	371	7	US-11-096-568A-26480	Sequence 26480, A	632	395	6	US-10-858-730-218	Sequence 218, App
560	6	0.8	371	7	US-11-096-568A-31791	Sequence 31791, A	633	395	6	US-10-467-657-4484	Sequence 4484, Ap
561	6	0.8	372	6	US-10-844-035-1	Sequence 1, Appl	634	395	7	US-11-072-175-235	Sequence 235, App
562	6	0.8	372	7	US-11-188-298-5057	Sequence 5057, Ap	635	396	7	US-11-188-298-3141	Sequence 3141, Ap
563	6	0.8	372	7	US-11-188-298-22470	Sequence 22470, A	636	396	7	US-11-120-543-10	Sequence 10, Appl
564	6	0.8	373	6	US-10-995-561-948	Sequence 948, App	637	396	7	US-11-096-568A-11143	Sequence 11143, A
565	6	0.8	373	6	US-11-082-389-200	Sequence 200, App	638	396	7	US-11-079-463-7583	Sequence 7583, Ap
566	6	0.8	373	7	US-11-087-099-8055	Sequence 8055, Ap	639	397	7	US-11-188-298-8578	Sequence 8578, Ap
567	6	0.8	373	7	US-11-096-568A-28149	Sequence 28149, A	640	397	7	US-11-216-267-34	Sequence 34, Appl
568	6	0.8	373	7	US-11-188-298-10929	Sequence 10929, A	641	397	7	US-11-232-382-34	Sequence 232, Appl
569	6	0.8	373	7	US-11-188-298-21280	Sequence 21280, A	642	398	6	US-10-517-939-210	Sequence 210, App
570	6	0.8	374	6	US-10-793-626-1356	Sequence 1356, Ap	643	398	7	US-11-096-568A-10967	Sequence 10967, A
571	6	0.8	374	7	US-11-096-568A-25555	Sequence 25555, A	644	398	7	US-11-096-568A-9672	Sequence 9672, Ap
572	6	0.8	374	7	US-11-079-463-9216	Sequence 9216, Ap	645	398	7	US-11-096-568A-9985	Sequence 9985, Ap
573	6	0.8	374	7	US-11-188-298-895	Sequence 895, App	646	399	6	US-11-188-298-1239	Sequence 1239, Ap
574	6	0.8	374	7	US-11-188-298-2309	Sequence 2309, Ap	647	399	7	US-11-051-568-27	Sequence 27, Appl
575	6	0.8	374	7	US-11-188-298-3366	Sequence 3366, Ap	648	399	7	US-11-051-568-27	Sequence 23, Appl
576	6	0.8	374	7	US-11-188-298-10019	Sequence 10019, A	649	399	7	US-11-236-555-23	Sequence 23, Appl
577	6	0.8	374	7	US-11-188-298-12373	Sequence 12373, A	650	399	7	US-11-096-568A-26912	Sequence 26912, A
578	6	0.8	375	6	US-10-995-561-946	Sequence 946, App	651	399	7	US-11-096-568A-29398	Sequence 29398, A
579	6	0.8	375	7	US-11-096-568A-26913	Sequence 26913, A	652	399	7	US-11-096-568A-31593	Sequence 31593, A
580	6	0.8	375	7	US-11-188-298-17154	Sequence 17154, A	653	399	7	US-11-096-568A-34046	Sequence 34046, A
581	6	0.8	375	7	US-11-188-298-17154	Sequence 17154, A	654	400	7	US-11-120-543-12	Sequence 12, Appl
582	6	0.8	376	6	US-11-188-298-22159	Sequence 22159, A	655	400	7	US-11-096-568A-27568	Sequence 27568, A
583	6	0.8	376	6	US-10-501-035-289	Sequence 289, App	656	401	7	US-11-096-568A-31592	Sequence 31592, A
584	6	0.8	376	7	US-11-169-041-143	Sequence 143, App	657	402	7	US-11-188-298-2264	Sequence 2264, Ap
585	6	0.8	376	7	US-11-188-298-717	Sequence 717, App	658	402	7	US-11-188-298-2750	Sequence 2750, Ap
586	6	0.8	377	7	US-11-096-568A-23007	Sequence 23007, A	659	403	7	US-11-188-298-13830	Sequence 13830, A
587	6	0.8	377	7	US-11-079-463-6182	Sequence 6182, Ap	660	403	7	US-11-188-298-14787	Sequence 14787, A
588	6	0.8	377	7	US-11-188-298-7208	Sequence 7208, Ap	661	404	7	US-11-188-298-661	Sequence 661, App
589	6	0.8	379	6	US-10-131-826A-328	Sequence 328, App	662	405	7	US-11-087-099-6553	Sequence 6553, Ap
590	6	0.8	379	6	US-10-858-730-22	Sequence 22, Appl	663	405	7	US-11-087-099-6553	Sequence 11442, A
591	6	0.8	379	6	US-10-525-674-6	Sequence 6, Appl	664	405	7	US-11-188-298-13339	Sequence 13339, A
592	6	0.8	379	6	US-10-973-115B-328	Sequence 328, App	665	406	7	US-11-096-568A-10009	Sequence 10009, A
593	6	0.8	379	7	US-11-087-099-5645	Sequence 5645, Ap	666	407	7	US-11-087-099-3465	Sequence 3465, Ap
594	6	0.8	379	7	US-11-087-099-11045	Sequence 11045, A	667	408	7	US-11-087-099-5495	Sequence 5495, Ap
595	6	0.8	379	7	US-11-096-568A-10010	Sequence 10010, A	668	408	7	US-11-087-099-9556	Sequence 9556, Ap
596	6	0.8	379	7	US-11-290-153-328	Sequence 328, App	669	409	6	US-11-087-099-9556	Sequence 55, Appl
597	6	0.8	380	7	US-11-144-833-12	Sequence 12, Appl	670	409	6	US-11-219-282-33	Sequence 33, Appl
598	6	0.8	380	7	US-11-144-833-13	Sequence 13, Appl	671	409	7	US-11-096-568A-28976	Sequence 28976, A
599	6	0.8	381	7	US-11-087-099-4409	Sequence 4409, Ap	672	410	6	US-10-467-657-4864	Sequence 4864, Ap
600	6	0.8	382	7	US-11-087-099-820	Sequence 820, App	673	410	7	US-11-096-568A-28998	Sequence 28998, A
601	6	0.8	382	7	US-11-096-568A-6376	Sequence 6376, Ap	674	410	7	US-11-188-298-12597	Sequence 12597, A
602	6	0.8	383	7	US-11-096-568A-9897	Sequence 9897, Ap	675	410	7	US-11-188-298-21575	Sequence 21575, A
603	6	0.8	384	7	US-11-120-543-2	Sequence 2, Appl	676	411	7	US-11-096-568A-29397	Sequence 29397, A
604	6	0.8	384	7	US-11-120-543-4	Sequence 4, Appl	677	412	7	US-11-096-568A-18897	Sequence 18897, A
605	6	0.8	384	7	US-11-120-543-6	Sequence 6, Appl	678	412	7	US-11-188-298-5342	Sequence 5342, Ap
606	6	0.8	384	7	US-11-120-543-8	Sequence 8, Appl	679	413	7	US-11-188-298-5513	Sequence 5513, Ap
607	6	0.8	384	7	US-11-120-543-14	Sequence 14, Appl	680	413	7	US-11-096-568A-13021	Sequence 13021, A
608	6	0.8	384	7	US-11-120-543-22	Sequence 22, Appl	681	415	6	US-11-096-568A-8947	Sequence 8947, Ap
609	6	0.8	384	7	US-11-096-568A-8948	Sequence 8948, Ap	682	415	7	US-11-096-568A-28148	Sequence 28148, A

683	6	0.8	417	7	US-11-096-568A-8397	Sequence 8397, Ap	756	6	0.8	463	7	US-11-087-099-2195	Sequence 2195, Ap
684	6	0.8	417	7	US-11-096-568A-28118	Sequence 28118, A	757	6	0.8	463	7	US-11-087-099-6438	Sequence 6438, Ap
685	6	0.8	418	7	US-11-186-284-187	Sequence 187, App	758	6	0.8	464	7	US-11-087-099-2888	Sequence 2888, Ap
686	6	0.8	419	7	US-11-096-568A-26911	Sequence 26911, A	759	6	0.8	464	7	US-11-087-099-4303	Sequence 4303, Ap
687	6	0.8	420	6	US-10-520-520-16	Sequence 14, Appl	760	6	0.8	464	7	US-11-087-099-6109	Sequence 6109, Ap
688	6	0.8	421	7	US-11-120-543-14	Sequence 16, Appl	761	6	0.8	464	7	US-11-188-298-14990	Sequence 14990, A
689	6	0.8	422	7	US-11-120-543-20	Sequence 20, Appl	762	6	0.8	464	7	US-11-188-298-16612	Sequence 16612, A
690	6	0.8	422	6	US-10-457-657-90	Sequence 90, Appl	763	6	0.8	467	7	US-11-188-298-17127	Sequence 17127, A
691	6	0.8	424	6	US-10-467-657-6344	Sequence 6344, Ap	764	6	0.8	469	7	US-11-072-512-2219	Sequence 2219, Ap
692	6	0.8	424	7	US-11-096-568A-19820	Sequence 19820, A	765	6	0.8	471	7	US-11-188-298-3821	Sequence 3821, Ap
693	6	0.8	427	7	US-11-188-298-7493	Sequence 7493, Ap	766	6	0.8	473	6	US-10-934-944-376	Sequence 376, App
694	6	0.8	428	7	US-11-096-568A-19819	Sequence 19819, A	767	6	0.8	473	6	US-10-934-944-381	Sequence 381, App
695	6	0.8	428	7	US-11-096-568A-31591	Sequence 31591, A	768	6	0.8	473	6	US-10-934-944-382	Sequence 382, App
696	6	0.8	428	7	US-11-188-298-19822	Sequence 19822, A	769	6	0.8	473	7	US-11-087-099-8304	Sequence 8304, Ap
697	6	0.8	429	7	US-11-188-298-5490	Sequence 5490, Ap	770	6	0.8	473	7	US-11-116-881A-2272	Sequence 2272, Ap
698	6	0.8	429	7	US-11-188-298-19897	Sequence 19897, A	771	6	0.8	473	7	US-11-116-881A-2278	Sequence 2278, Ap
699	6	0.8	430	7	US-11-172-740-331	Sequence 331, App	772	6	0.8	473	7	US-11-116-881A-2300	Sequence 2300, Ap
700	6	0.8	430	7	US-11-172-740-330	Sequence 330, App	773	6	0.8	473	7	US-11-188-298-1307	Sequence 1307, Ap
701	6	0.8	430	7	US-11-188-298-3502	Sequence 3502, Ap	774	6	0.8	473	7	US-11-188-298-2143	Sequence 2143, Ap
702	6	0.8	430	7	US-11-188-298-14611	Sequence 14611, A	775	6	0.8	473	7	US-11-188-298-4129	Sequence 4129, Ap
703	6	0.8	431	6	US-10-525-674-26	Sequence 26, Appl	776	6	0.8	473	7	US-11-188-298-4172	Sequence 4172, Ap
704	6	0.8	431	7	US-11-188-298-5792	Sequence 5792, Ap	777	6	0.8	473	7	US-11-188-298-12250	Sequence 12250, A
705	6	0.8	431	7	US-11-188-298-9889	Sequence 9889, Ap	778	6	0.8	473	7	US-11-188-298-13095	Sequence 13095, A
706	6	0.8	431	7	US-11-188-298-12175	Sequence 12175, A	779	6	0.8	473	7	US-11-188-298-18298	Sequence 18298, A
707	6	0.8	431	7	US-11-188-298-13508	Sequence 13508, A	780	6	0.8	474	7	US-11-188-298-667	Sequence 667, App
708	6	0.8	432	7	US-11-087-099-704	Sequence 704, App	781	6	0.8	474	7	US-11-188-298-5955	Sequence 5955, Ap
709	6	0.8	432	7	US-11-087-099-10706	Sequence 10706, A	782	6	0.8	474	7	US-11-188-298-14126	Sequence 14126, A
710	6	0.8	432	7	US-11-096-568A-25141	Sequence 25141, A	783	6	0.8	474	7	US-11-188-298-22242	Sequence 22242, A
711	6	0.8	432	7	US-11-188-298-19037	Sequence 19037, A	784	6	0.8	474	7	US-11-188-298-22303	Sequence 22303, A
712	6	0.8	434	7	US-11-196-475-164	Sequence 164, App	785	6	0.8	475	6	US-10-510-386-98	Sequence 98, Appl
713	6	0.8	436	7	US-11-087-099-11529	Sequence 11529, A	786	6	0.8	475	7	US-11-087-099-2709	Sequence 2709, Ap
714	6	0.8	436	7	US-11-188-298-22548	Sequence 22548, A	787	6	0.8	475	7	US-11-188-298-2476	Sequence 2476, Ap
715	6	0.8	437	7	US-11-073-626-1	Sequence 1, Appl	788	6	0.8	475	7	US-11-188-298-2585	Sequence 2585, Ap
716	6	0.8	437	7	US-11-087-099-3654	Sequence 3654, Ap	789	6	0.8	476	7	US-11-188-298-18547	Sequence 18547, A
717	6	0.8	437	7	US-11-188-298-19155	Sequence 19155, A	790	6	0.8	476	7	US-11-096-568A-15793	Sequence 15793, A
718	6	0.8	438	7	US-11-096-568A-30832	Sequence 30832, A	791	6	0.8	477	7	US-11-087-099-8801	Sequence 8801, A
719	6	0.8	439	7	US-11-079-463-6330	Sequence 6330, Ap	792	6	0.8	479	7	US-11-096-568A-19818	Sequence 19818, A
720	6	0.8	439	7	US-11-079-463-8028	Sequence 8028, Ap	793	6	0.8	479	7	US-11-096-568A-28975	Sequence 28975, A
721	6	0.8	439	7	US-11-188-298-3673	Sequence 3673, Ap	794	6	0.8	479	7	US-11-188-298-12225	Sequence 12225, A
722	6	0.8	440	7	US-11-072-512-3856	Sequence 3856, Ap	795	6	0.8	480	7	US-11-096-568A-26612	Sequence 26612, A
723	6	0.8	440	7	US-11-188-298-10114	Sequence 10114, A	796	6	0.8	482	7	US-11-055-822-20	Sequence 20, Appl
724	6	0.8	442	6	US-10-513-639-25	Sequence 25, Appl	797	6	0.8	482	7	US-11-096-568A-9895	Sequence 9895, Ap
725	6	0.8	442	6	US-10-506-454-1590	Sequence 1590, Ap	798	6	0.8	482	7	US-11-096-568A-12959	Sequence 12959, A
726	6	0.8	442	6	US-10-521-720-1734	Sequence 1734, Ap	799	6	0.8	482	7	US-11-188-298-6868	Sequence 6868, Ap
727	6	0.8	444	6	US-10-467-657-2414	Sequence 2414, Ap	800	6	0.8	483	7	US-11-087-099-9313	Sequence 9313, Ap
728	6	0.8	445	7	US-11-074-176-182	Sequence 182, App	801	6	0.8	483	7	US-11-096-568A-18833	Sequence 18833, A
729	6	0.8	446	7	US-11-188-298-3929	Sequence 3929, Ap	802	6	0.8	483	7	US-11-188-298-19672	Sequence 19672, A
730	6	0.8	447	7	US-11-096-568A-26613	Sequence 26613, A	803	6	0.8	484	7	US-11-188-298-13873	Sequence 13873, A
731	6	0.8	447	7	US-11-096-568A-28117	Sequence 28117, A	804	6	0.8	485	6	US-10-501-035-349	Sequence 349, App
732	6	0.8	448	7	US-11-188-298-11427	Sequence 11427, A	805	6	0.8	485	7	US-11-055-822-18	Sequence 18, Appl
733	6	0.8	449	7	US-11-087-099-11350	Sequence 11350, A	806	6	0.8	486	7	US-11-087-099-9830	Sequence 9830, Ap
734	6	0.8	450	7	US-11-188-298-336	Sequence 336, App	807	6	0.8	486	7	US-11-079-463-8878	Sequence 8878, Ap
735	6	0.8	450	7	US-11-188-298-12480	Sequence 12480, A	808	6	0.8	486	7	US-11-188-298-11517	Sequence 11517, A
736	6	0.8	451	7	US-11-087-099-1581	Sequence 1581, Ap	809	6	0.8	486	7	US-11-188-298-17433	Sequence 17433, A
737	6	0.8	451	7	US-11-096-568A-9896	Sequence 9896, Ap	810	6	0.8	486	7	US-11-188-298-21031	Sequence 21031, A
738	6	0.8	452	7	US-11-188-298-9746	Sequence 9746, Ap	811	6	0.8	486	7	US-11-188-298-21597	Sequence 21597, A
739	6	0.8	453	6	US-10-467-657-1642	Sequence 1642, Ap	812	6	0.8	487	7	US-11-087-099-3264	Sequence 3264, Ap
740	6	0.8	453	7	US-11-096-568A-27953	Sequence 27953, A	813	6	0.8	487	7	US-11-188-298-6934	Sequence 6934, Ap
741	6	0.8	453	7	US-11-188-298-13421	Sequence 13421, A	814	6	0.8	487	7	US-11-188-298-13142	Sequence 13142, A
742	6	0.8	453	7	US-11-188-298-20441	Sequence 20441, A	815	6	0.8	488	7	US-11-188-298-8600	Sequence 8600, Ap
743	6	0.8	454	7	US-11-087-099-12184	Sequence 12184, A	816	6	0.8	488	7	US-11-188-298-9657	Sequence 9657, Ap
744	6	0.8	455	7	US-11-087-099-8847	Sequence 8847, Ap	817	6	0.8	489	7	US-11-188-298-9657	Sequence 9657, Ap
745	6	0.8	456	7	US-11-098-686-11117	Sequence 11117, A	818	6	0.8	490	7	US-11-096-568A-31601	Sequence 31601, A
746	6	0.8	457	7	US-11-246-793-2	Sequence 2, Appl	819	6	0.8	490	7	US-11-188-298-3993	Sequence 3993, Ap
747	6	0.8	457	7	US-11-246-793-48	Sequence 48, Appl	820	6	0.8	490	7	US-11-188-298-6814	Sequence 6814, Ap
748	6	0.8	457	7	US-11-246-793-50	Sequence 50, Appl	821	6	0.8	490	7	US-11-188-298-9922	Sequence 9922, Ap
749	6	0.8	458	6	US-10-454-437-340	Sequence 340, App	822	6	0.8	491	7	US-11-205-109-21	Sequence 21, Appl
750	6	0.8	459	7	US-11-188-298-19083	Sequence 19083, A	823	6	0.8	493	7	US-11-087-099-11095	Sequence 11095, A
751	6	0.8	461	6	US-10-934-944-176	Sequence 176, App	824	6	0.8	493	7	US-11-188-298-7250	Sequence 7250, Ap
752	6	0.8	461	7	US-11-116-881A-185	Sequence 185, App	825	6	0.8	495	6	US-10-467-9628-93	Sequence 93, Appl
753	6	0.8	462	7	US-11-087-099-2409	Sequence 2409, Ap	826	6	0.8	495	7	US-11-087-099-3528	Sequence 3528, Ap
754	6	0.8	463	7	US-11-128-900-4	Sequence 4, Appl	827	6	0.8	495	7	US-11-087-099-11944	Sequence 11944, A
755	6	0.8	463	7	US-11-128-900-68	Sequence 68, Appl	828	6	0.8	495	7	US-11-188-298-22312	Sequence 22312, A



829	6	0.8	496	7	US-11-096-568A-31600	Sequence 31600, A	902	6	0.8	549	7	US-11-188-298-5783	Sequence 5783, Ap
830	6	0.8	496	7	US-11-079-463-9399	Sequence 9399, Ap	903	6	0.8	551	7	US-11-079-463-8767	Sequence 8767, Ap
831	6	0.8	498	7	US-11-188-298-8378	Sequence 8378, Ap	904	6	0.8	554	7	US-11-188-298-2588	Sequence 2588, Ap
832	6	0.8	498	7	US-11-188-298-16314	Sequence 16314, A	905	6	0.8	555	7	US-11-188-298-20131	Sequence 20131, A
833	6	0.8	498	7	US-11-188-298-20979	Sequence 20979, A	906	6	0.8	555	7	US-11-188-298-22563	Sequence 22563, A
834	6	0.8	499	7	US-11-188-298-6962	Sequence 6962, Ap	907	6	0.8	556	6	US-10-467-657-498	Sequence 498, App
835	6	0.8	500	7	US-11-087-099-9861	Sequence 9861, Ap	908	6	0.8	556	6	US-10-467-657-498	Sequence 498, App
836	6	0.8	500	7	US-11-087-099-12411	Sequence 12411, A	909	6	0.8	557	6	US-11-188-298-20249	Sequence 20249, A
837	6	0.8	500	7	US-11-096-568A-18410	Sequence 18410, A	910	6	0.8	557	6	US-10-467-657-2888	Sequence 2888, Ap
838	6	0.8	500	7	US-11-096-568A-32877	Sequence 32877, A	911	6	0.8	558	7	US-11-096-568A-34045	Sequence 34045, A
839	6	0.8	502	7	US-11-199-233-13	Sequence 13, Appl	912	6	0.8	559	7	US-11-188-298-986	Sequence 986, App
840	6	0.8	503	7	US-11-082-389-290	Sequence 290, App	913	6	0.8	560	7	US-11-096-568A-18831	Sequence 18831, A
841	6	0.8	504	6	US-10-934-944-178	Sequence 178, App	914	6	0.8	562	6	US-10-506-454-1299	Sequence 1299, A
842	6	0.8	504	7	US-11-116-881A-187	Sequence 187, Appl	915	6	0.8	562	7	US-11-096-568A-30550	Sequence 30550, A
843	6	0.8	505	6	US-10-763-712A-26	Sequence 26, Appl	916	6	0.8	563	7	US-11-055-822-254	Sequence 254, App
844	6	0.8	505	6	US-10-763-712A-88	Sequence 88, Appl	917	6	0.8	565	7	US-11-087-099-3971	Sequence 3971, Ap
845	6	0.8	505	6	US-10-763-712A-123	Sequence 123, App	918	6	0.8	565	7	US-11-072-512-3772	Sequence 3772, Ap
846	6	0.8	505	7	US-11-079-463-8719	Sequence 8719, Ap	919	6	0.8	567	7	US-11-188-298-929	Sequence 929, App
847	6	0.8	505	7	US-10-873-528-80	Sequence 80, Appl	920	6	0.8	567	7	US-11-185-342-15	Sequence 15, Appl
848	6	0.8	506	6	US-11-087-099-10758	Sequence 10758, A	921	6	0.8	568	7	US-11-188-298-2752	Sequence 2752, Ap
849	6	0.8	506	7	US-11-096-568A-34051	Sequence 34051, A	922	6	0.8	568	7	US-11-188-298-4524	Sequence 4524, Ap
850	6	0.8	507	7	US-11-096-568A-18409	Sequence 18409, A	923	6	0.8	568	7	US-11-188-298-14329	Sequence 14329, A
851	6	0.8	507	7	US-11-096-568A-32876	Sequence 32876, A	924	6	0.8	568	7	US-11-188-298-22054	Sequence 22054, A
852	6	0.8	507	7	US-11-188-298-11793	Sequence 11793, A	925	6	0.8	572	7	US-11-096-568A-12957	Sequence 12957, A
853	6	0.8	509	6	US-10-793-626-98	Sequence 98, Appl	926	6	0.8	573	7	US-11-188-298-14241	Sequence 14241, A
854	6	0.8	510	7	US-11-087-099-1859	Sequence 1859, Ap	927	6	0.8	574	6	US-10-517-939-108	Sequence 108, App
855	6	0.8	510	7	US-11-188-298-12808	Sequence 12808, A	928	6	0.8	575	7	US-11-188-298-1157	Sequence 1157, Ap
856	6	0.8	510	7	US-11-087-099-7567	Sequence 7567, Ap	929	6	0.8	575	7	US-11-188-298-3182	Sequence 3182, Ap
857	6	0.8	511	7	US-11-087-099-17979	Sequence 17979, A	930	6	0.8	576	7	US-11-096-568A-8957	Sequence 8957, Ap
858	6	0.8	511	7	US-11-188-298-19503	Sequence 19503, A	931	6	0.8	576	7	US-11-096-568A-8959	Sequence 8959, Ap
859	6	0.8	511	7	US-11-188-298-5209	Sequence 5209, Ap	932	6	0.8	583	7	US-11-079-463-9397	Sequence 9397, Ap
860	6	0.8	512	7	US-11-087-099-4771	Sequence 4771, Ap	933	6	0.8	585	7	US-11-188-298-6205	Sequence 6205, Ap
861	6	0.8	512	7	US-11-188-298-4771	Sequence 4771, Ap	934	6	0.8	587	7	US-11-079-463-8026	Sequence 8026, A
862	6	0.8	513	6	US-10-934-944-272	Sequence 272, App	935	6	0.8	587	7	US-11-188-298-20209	Sequence 20209, A
863	6	0.8	513	7	US-11-135-667-63	Sequence 63, Appl	936	6	0.8	587	7	US-11-079-463-5824	Sequence 5824, Ap
864	6	0.8	513	7	US-11-116-881A-281	Sequence 281, App	937	6	0.8	595	7	US-11-188-298-17934	Sequence 17934, A
865	6	0.8	514	7	US-11-188-298-10977	Sequence 10977, A	938	6	0.8	597	6	US-10-613-744-7	Sequence 7, Appl
866	6	0.8	514	7	US-11-235-621-17	Sequence 17, Appl	939	6	0.8	599	7	US-11-188-298-17505	Sequence 17505, A
867	6	0.8	515	7	US-11-087-099-4968	Sequence 4968, Ap	940	6	0.8	599	7	US-11-188-298-18272	Sequence 18272, A
868	6	0.8	517	7	US-11-188-298-19638	Sequence 238, App	941	6	0.8	599	7	US-11-188-298-18272	Sequence 18272, A
869	6	0.8	518	6	US-10-934-944-298	Sequence 307, App	942	6	0.8	601	7	US-11-098-686-10933	Sequence 10933, A
870	6	0.8	518	7	US-11-116-881A-307	Sequence 307, App	943	6	0.8	602	6	US-10-493-509-51	Sequence 51, Appl
871	6	0.8	519	6	US-10-485-517-220	Sequence 220, App	944	6	0.8	602	7	US-11-072-512-3092	Sequence 3092, Ap
872	6	0.8	519	7	US-11-188-298-4344	Sequence 4344, Ap	945	6	0.8	604	7	US-11-216-267-8	Sequence 8, Appl
873	6	0.8	519	7	US-11-188-298-21708	Sequence 21708, A	946	6	0.8	604	7	US-11-232-382-8	Sequence 8, Appl
874	6	0.8	520	7	US-11-188-298-4143	Sequence 4143, Ap	947	6	0.8	605	6	US-10-821-234-1207	Sequence 30549, A
875	6	0.8	521	7	US-11-096-568A-26611	Sequence 26611, A	948	6	0.8	608	7	US-11-096-568A-30549	Sequence 10137, A
876	6	0.8	521	7	US-11-096-568A-34050	Sequence 18408, A	949	6	0.8	608	7	US-11-087-099-10631	Sequence 14625, A
877	6	0.8	525	7	US-11-096-568A-18408	Sequence 18408, A	950	6	0.8	610	7	US-11-188-298-14425	Sequence 8994, Ap
878	6	0.8	527	7	US-11-096-568A-32875	Sequence 32875, A	951	6	0.8	612	7	US-11-087-099-8984	Sequence 8984, Ap
879	6	0.8	528	7	US-11-087-099-7839	Sequence 7839, Ap	952	6	0.8	617	7	US-11-096-568A-8956	Sequence 8956, Ap
880	6	0.8	529	7	US-11-087-099-1839	Sequence 1839, Ap	953	6	0.8	619	7	US-11-087-099-381	Sequence 229, App
881	6	0.8	530	7	US-11-096-568A-15792	Sequence 15792, A	954	6	0.8	619	7	US-11-087-099-381	Sequence 381, App
882	6	0.8	530	7	US-11-096-568A-28974	Sequence 28974, A	955	6	0.8	619	7	US-11-096-568A-28116	Sequence 28116, A
883	6	0.8	532	7	US-11-087-099-12403	Sequence 12403, A	956	6	0.8	621	6	US-10-632-150-56	Sequence 56, Appl
884	6	0.8	533	7	US-11-087-099-12358	Sequence 12358, A	957	6	0.8	621	7	US-11-073-457-56	Sequence 56, Appl
885	6	0.8	533	7	US-11-188-298-17096	Sequence 17096, A	958	6	0.8	621	7	US-11-073-457-56	Sequence 56, Appl
886	6	0.8	534	7	US-11-096-568A-31599	Sequence 31599, A	959	6	0.8	621	7	US-11-073-457-56	Sequence 56, Appl
887	6	0.8	535	6	US-10-131-826A-124	Sequence 124, App	960	6	0.8	624	6	US-10-467-657-338	Sequence 338, App
888	6	0.8	535	6	US-10-973-115B-124	Sequence 124, App	961	6	0.8	624	6	US-11-087-099-8127	Sequence 8127, Ap
889	6	0.8	535	7	US-11-290-153-154	Sequence 153, Appl	962	6	0.8	629	7	US-11-079-463-7386	Sequence 7386, Ap
890	6	0.8	537	6	US-10-793-626-1712	Sequence 1712, Ap	963	6	0.8	631	7	US-11-188-298-3431	Sequence 3431, Ap
891	6	0.8	537	6	US-11-098-686-10170	Sequence 10170, A	964	6	0.8	631	7	US-11-188-298-4923	Sequence 4923, Ap
892	6	0.8	540	7	US-11-188-298-1758	Sequence 1758, Ap	965	6	0.8	631	7	US-11-188-298-21358	Sequence 21358, A
893	6	0.8	541	7	US-11-096-568A-12958	Sequence 12958, A	966	6	0.8	632	7	US-11-079-463-5795	Sequence 5795, Ap
894	6	0.8	542	7	US-11-188-298-1678	Sequence 1678, Ap	967	6	0.8	633	7	US-11-188-298-3895	Sequence 3895, Ap
895	6	0.8	545	7	US-11-096-568A-15791	Sequence 15791, A	968	6	0.8	633	7	US-11-188-298-782	Sequence 8147, Ap
896	6	0.8	547	6	US-10-770-726-87	Sequence 87, Appl	969	6	0.8	634	7	US-11-087-099-8147	Sequence 8147, Ap
897	6	0.8	547	6	US-11-096-568A-34049	Sequence 34049, A	970	6	0.8	637	7	US-11-175-690-558	Sequence 222, App
898	6	0.8	547	7	US-11-096-070-2	Sequence 2, Appl	971	6	0.8	639	7	US-11-074-176-222	Sequence 7258, Ap
899	6	0.8	549	7	US-11-096-070-6	Sequence 6, Appl	972	6	0.8	646	7	US-11-079-463-7258	Sequence 2596, Ap
900	6	0.8	549	7	US-11-096-070-6	Sequence 6, Appl	973	6	0.8	650	7	US-11-087-099-2596	Sequence 55, Appl
901	6	0.8	549	7	US-11-096-070-8	Sequence 8, Appl	974	6	0.8	653	7	US-11-137-465-55	Sequence 55, Appl

```
975 6 0.8 654 7 US-11-079-463-6150 Sequence 6150, Ap
976 6 0.8 654 7 US-11-188-298-13949 Sequence 13949, A
977 6 0.8 658 7 US-11-079-463-9653 Sequence 9653, Ap
978 6 0.8 658 7 US-11-079-463-9783 Sequence 9783, Ap
979 6 0.8 665 7 US-11-124-368A-289 Sequence 289, App
980 6 0.8 668 6 US-10-467-657-5042 Sequence 5042, Ap
981 6 0.8 688 7 US-11-188-298-1144 Sequence 1144, Ap
982 6 0.8 669 7 US-11-087-099-1120 Sequence 1120, Ap
983 6 0.8 670 7 US-11-188-298-15016 Sequence 15016, A
984 6 0.8 671 6 US-10-506-454-88 Sequence 88, Appl
985 6 0.8 676 7 US-11-098-686-10486 Sequence 10486, A
986 6 0.8 684 7 US-11-188-298-8055 Sequence 8055, Ap
987 6 0.8 687 6 US-10-714-887-268 Sequence 268, App
988 6 0.8 689 7 US-11-079-463-6382 Sequence 6382, Ap
989 6 0.8 692 7 US-11-052-554A-213 Sequence 213, App
990 6 0.8 692 7 US-11-188-298-5840 Sequence 5840, Ap
991 6 0.8 697 7 US-11-052-554A-110 Sequence 110, App
992 6 0.8 698 7 US-11-079-463-6720 Sequence 6720, Ap
993 6 0.8 699 7 US-11-152-601-21 Sequence 21, Appl
994 6 0.8 699 7 US-11-235-621-9 Sequence 9, Appl1
995 6 0.8 700 7 US-11-098-686-10793 Sequence 10793, A
996 6 0.8 701 7 US-11-235-621-1 Sequence 1, Appl1
997 6 0.8 702 7 US-11-188-298-12930 Sequence 12930, A
998 6 0.8 703 7 US-11-079-463-6948 Sequence 6948, Ap
999 6 0.8 703 7 US-11-188-298-16110 Sequence 16110, A
1000 6 0.8 713 7 US-11-188-298-18086 Sequence 18086, A
```

## ALIGNMENTS

```
RESULT 1
US-10-467-657-6026
; Sequence 6026, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO 6026
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6026

Query Match 26.3%; Score 210; DB 6; Length 792;
Best Local Similarity 100.0%; Pred. No. 1.5e-206;
Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLKQTASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Db 1 MKLKQTASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60

QY 61 IIKSLVATGFFDVRVETADGQLLTVIERPTTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
Db 61 IIKSLVATGFFDVRVETADGQLLTVIERPTTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120

QY 121 SOYFNOATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITDIE 180
Db 121 SOYFNOATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITDIE 180

QY 181 FEGNQVYSDRKLQMSLTGGIWTWLTTRS 210
Db 181 FEGNQVYSDRKLQMSLTGGIWTWLTTRS 210

;
;
; ORGANISM: Neisseria gonorrhoeae
```

```
Db 181 FEGNQVYSDRKLQMSLTGGIWTWLTTRS 210

RESULT 2
US-10-467-657-7528
; Sequence 7528, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO 7528
; LENGTH: 792
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7528
```

```
Query Match 26.3%; Score 210; DB 6; Length 792;
Best Local Similarity 100.0%; Pred. No. 1.5e-206;
Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MKLKQTASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Db 1 MKLKQTASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60

QY 61 IIKSLVATGFFDVRVETADGQLLTVIERPTTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
Db 61 IIKSLVATGFFDVRVETADGQLLTVIERPTTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120

QY 121 SOYFNOATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITDIE 180
Db 121 SOYFNOATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITDIE 180

QY 181 FEGNQVYSDRKLQMSLTGGIWTWLTTRS 210
Db 181 FEGNQVYSDRKLQMSLTGGIWTWLTTRS 210

;
;
; ORGANISM: Neisseria gonorrhoeae
```

```
RESULT 3
US-11-103-957-92
; Sequence 92, Application US/11103957
; Publication No. US20050281847A1
; GENERAL INFORMATION:
; APPLICANT: Berthet, Francois-Xavier Jacques
; APPLICANT: Lobet, Yves
; APPLICANT: Foolman, Jan
; APPLICANT: Verlant, Vincent Georges Christian Louis
; TITLE OF INVENTION: Vaccine Composition
; FILE REFERENCE: B45261
; CURRENT APPLICATION NUMBER: US/11/103,957
; CURRENT FILING DATE: 2005-04-12
; PRIOR APPLICATION NUMBER: US/10/467,534
; PRIOR FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: PCT/EP02/01356
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: GB 0103169.9
; PRIOR FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 792
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
```

```
US-11-103-957-92
Query Match      19.7%; Score 157; DB 7; Length 792;
Best Local Similarity 100.0%; Pred. No. 3.5e-152;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 332 TKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVVRRELROMESAPYDTSKLQSKERVEL 391
Db 332 TKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVVRRELROMESAPYDTSKLQSKERVEL 391
Qy 392 LGYFDNVQFQDAVPLAGTPDKVDLNMSLTERSTGSLDLSAGVQDTGLVMSAGVSQDNLFG 451
Db 392 LGYFDNVQFQDAVPLAGTPDKVDLNMSLTERSTGSLDLSAGVQDTGLVMSAGVSQDNLFG 451
Qy 452 TGKSAALRASRSKTTLNGSLSFDPYFTADGVSLGYD 488
Db 452 TGKSAALRASRSKTTLNGSLSFDPYFTADGVSLGYD 488

RESULT 4
US-10-506-454-1658
; Sequence 1658, Application US/10506454
; Publication No. US20060068386A1
; GENERAL INFORMATION:
; APPLICANT: Slesarev, Alexi I
; APPLICANT: Mezhevaya, Katja V
; APPLICANT: Polushin, Nikolai N
; APPLICANT: Shcherbinina, Olga V
; APPLICANT: Shakhova, Vera V
; APPLICANT: Malykh, Andrei G
; APPLICANT: Kozayvkin, Sergei A
; TITLE OF INVENTION: The Complete Genome and Protein Sequences of the Hyperthermophile
; TITLE OF INVENTION: Methanopyrus Kandleri AV19 and Monophyly of Archaeal Methanogens
; TITLE OF INVENTION: and Methods of Use Thereof
; FILE REFERENCE: FID001
; CURRENT APPLICATION NUMBER: US/10/506,454
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/US03/06664
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: 60/361,742
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 1722
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1658
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Methanopyrus kandleri
US-10-506-454-1658

Query Match      0.9%; Score 7; DB 6; Length 102;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 764 LSPGLGPM 770
Db 25 LSPGLGPM 31

RESULT 5
US-11-158-655-6
; Sequence 6, Application US/11158655
; Publication No. US20060037089A1
; GENERAL INFORMATION:
; APPLICANT: TSAI, MINDY
; APPLICANT: TAM, SEE-YING
; APPLICANT: GALLI, STEPHEN J
; TITLE OF INVENTION: IN VIVO MODELS FOR RABGEF1- DEPENDENT
; TITLE OF INVENTION: SIGNALING AND FUNCTIONS
; FILE REFERENCE: STAN-371
; CURRENT APPLICATION NUMBER: US/11/158,655
; CURRENT FILING DATE: 2005-06-21
; PRIOR APPLICATION NUMBER: 60/582,755
; PRIOR FILING DATE: 2004-06-24
```

```
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Yeast
US-11-158-655-6

Query Match      0.9%; Score 7; DB 7; Length 147;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 416 MSLTERS 422
Db 140 MSLTERS 146

RESULT 6
US-11-087-099-3827
; Sequence 3827, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 3827
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Oceanobacillus ihayensis HTE831
US-11-087-099-3827

Query Match      0.9%; Score 7; DB 7; Length 157;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 210 SNOFNEQ 216
Db 63 SNOFNEQ 69

RESULT 7
US-11-172-740-872
; Sequence 872, Application US/11172740
; Publication No. US20060057724A1
; GENERAL INFORMATION:
; APPLICANT: MASCIA, Peter
; APPLICANT: ALEXANDROV, Nikolai
; APPLICANT: BROVER, Vyacheslav
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY USEFUL FOR
; TITLE OF INVENTION: PLANT CHARACTERISTICS AND PHENOTYPES
; FILE REFERENCE: 2750-1602PUS2
; CURRENT APPLICATION NUMBER: US/11/172,740
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/583,621
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/584,829
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/584,800
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 2523
; SEQ ID NO 872
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (17)..(80)
; OTHER INFORMATION: Pfam Name: AP2; Pfam Description: AP2 domain
; FEATURE:
; NAME/KEY: misc_feature
```

```
; LOCATION: (17)..(80)
; OTHER INFORMATION: Pfam Name: AP2; Pfam Description: AP2 domain
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Utility: Useful for delaying flowering time
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Utility: Useful for making larger plants
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Utility: Useful for making plants with increased biomass and foli
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Utility: Useful for making smaller plants
; US-11-172-740-872

Query Match          0.9%; Score 7; DB 7; Length 177;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 465 TTTLGSL 471
Db 136 TTTLGSL 142

RESULT 8
US-11-096-568A-1873
; Sequence 1873, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 1873
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(222)
; OTHER INFORMATION: Ceres Seq. ID no. 15179541
US-11-096-568A-1873

Query Match          0.9%; Score 7; DB 7; Length 222;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 729 SATGGRV 735
Db 216 SATGGRV 222

RESULT 9
US-11-096-568A-27201
; Sequence 27201, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27201
```

```
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(222)
; OTHER INFORMATION: Ceres Seq. ID no. 15179541
US-11-096-568A-27201

Query Match          0.9%; Score 7; DB 7; Length 222;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 729 SATGGRV 735
Db 216 SATGGRV 222

RESULT 10
US-11-188-298-16796
; Sequence 16796, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 16796
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Pachysandra terminalis
US-11-188-298-16796

Query Match          0.9%; Score 7; DB 7; Length 238;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 RVEGLQR 35
Db 95 RVEGLQR 101

RESULT 11
US-11-096-568A-1872
; Sequence 1872, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 1872
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(241)
; OTHER INFORMATION: Ceres Seq. ID no. 15179540
US-11-096-568A-1872

Query Match          0.9%; Score 7; DB 7; Length 241;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 729 SATGGRV 735
```

```
Db      235 SATGRV 241
|||||
RESULT 12
US-11-096-568A-27200
; Sequence 27200, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27200
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(241)
; OTHER INFORMATION: Ceres Seq. ID no. 15179540
US-11-096-568A-27200

Query Match      0.9%; Score 7; DB 7; Length 241;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      729 SATGRV 735
|||||
Db      235 SATGRV 241

RESULT 13
US-11-079-463-6578
; Sequence 6578, Application US/11079463
; Publication No. US20060073161A1
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTERIOIDES FR
; FILE REFERENCE: PATH00-03DIV2
; CURRENT APPLICATION NUMBER: US/11/079,463
; CURRENT FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/128,705
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/540,209
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 6578
; LENGTH: 286
; TYPE: PRT
; ORGANISM: B.fragilis
US-11-079-463-6578

Query Match      0.9%; Score 7; DB 7; Length 286;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      481 DGVSLGY 487
|||||
Db      110 DGVSLGY 116

RESULT 14
US-11-096-568A-18041
; Sequence 18041, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 18041
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(287)
; OTHER INFORMATION: Ceres Seq. ID no. 12362473
US-11-096-568A-18041

Query Match      0.9%; Score 7; DB 7; Length 287;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      451 GTGKSAA 457
|||||
Db      211 GTGKSAA 217

RESULT 15
US-11-188-298-10985
; Sequence 10985, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 10985
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Cicer arietinum
US-11-188-298-10985

Query Match      0.9%; Score 7; DB 7; Length 308;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      324 VOPLPNA 330
|||||
Db      207 VOPLPNA 213

Search completed: April 12, 2006, 16:38:40
Job time : 32 secs
```

**This Page Blank (uspto)**

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 12, 2006, 16:34:33 ; Search time 171 Seconds  
(without alignment)  
1947.427 Million cell updates/sec

Title: US-10-606-618-4

Perfect score: 797

Sequence: 1 MKLKQIASALMLGISPLAF.....LKKPDEIQRFOQLGTTT 797

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 1867569 seqs, 417829326 residues

Word size : 1

Total number of hits satisfying chosen parameters: 1864806

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Published Applications AA Main:

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	797	100.0	797	3	US-09-994-192-4
2	797	100.0	797	5	US-10-606-618-4
3	752	94.4	797	4	US-10-181-660-3
4	752	94.4	797	4	US-10-181-660-11
5	752	94.4	797	4	US-10-320-800-6
6	752	94.4	797	5	US-10-181-600-3
7	752	94.4	797	5	US-10-181-600-11
8	752	94.4	797	5	US-10-988-943-7
9	751	94.2	776	4	US-10-181-660-5
10	751	94.2	776	4	US-10-181-660-13
11	751	94.2	776	5	US-10-181-600-5
12	751	94.2	776	5	US-10-181-600-13
13	210	26.3	792	4	US-10-181-660-7
14	210	26.3	792	5	US-10-181-600-7
15	189	23.7	771	4	US-10-181-660-9
16	189	23.7	771	5	US-10-181-660-9
17	157	19.7	792	3	US-09-994-192-2
18	157	19.7	792	4	US-10-467-534-92
19	157	19.7	792	5	US-10-606-618-2
20	21	2.6	21	4	US-10-181-660-8
21	21	2.6	21	5	US-10-181-600-8
22	19	2.4	21	4	US-10-181-660-4
23	19	2.4	21	5	US-10-181-600-4
24	15	1.9	15	4	US-10-181-660-1
25	15	1.9	15	5	US-10-181-600-1
26	11	1.4	21	4	US-10-181-660-12
27	11	1.4	21	5	US-10-181-600-12

28	9	1.1	177	4	US-10-425-114-63291	Sequence 63291, A
29	9	1.1	246	4	US-10-424-599-149837	Sequence 149837, A
30	9	1.1	381	4	US-10-437-963-154779	Sequence 154779, A
31	9	1.1	408	4	US-10-425-114-72370	Sequence 72370, A
32	9	1.1	408	4	US-10-425-115-266878	Sequence 266878, A
33	9	1.1	443	4	US-10-424-599-14939	Sequence 147939, A
34	9	1.1	1035	4	US-10-389-566-2330	Sequence 2330, A
35	8	1.0	97	3	US-09-933-767-1092	Sequence 1092, A
36	8	1.0	97	4	US-10-004-860-1092	Sequence 1092, A
37	8	1.0	97	4	US-10-023-282-1092	Sequence 168144, A
38	8	1.0	104	4	US-10-437-963-168144	Sequence 217994, A
39	8	1.0	154	4	US-10-424-599-171994	Sequence 4323, A
40	8	1.0	216	4	US-10-369-493-4323	Sequence 51162, A
41	8	1.0	250	4	US-10-425-114-51162	Sequence 46228, A
42	8	1.0	266	5	US-10-450-763-46228	Sequence 4240, A
43	8	1.0	299	3	US-09-738-626-4240	Sequence 13893, A
44	8	1.0	315	4	US-10-369-493-13893	Sequence 146233, A
45	8	1.0	367	4	US-10-437-963-146233	Sequence 146233, A
46	8	1.0	422	4	US-10-369-493-12887	Sequence 14887, A
47	8	1.0	445	5	US-10-450-763-48222	Sequence 48222, A
48	8	1.0	494	4	US-10-369-493-13128	Sequence 13128, A
49	8	1.0	583	4	US-10-389-647-479	Sequence 479, A
50	8	1.0	745	5	US-10-450-763-34211	Sequence 34211, A
51	8	1.0	745	5	US-10-450-763-39468	Sequence 39468, A
52	8	1.0	745	5	US-10-450-763-40726	Sequence 40726, A
53	8	1.0	785	4	US-10-450-763-45249	Sequence 45249, A
54	8	1.0	882	4	US-10-437-963-201769	Sequence 201769, A
55	8	1.0	897	5	US-10-437-963-118138	Sequence 118138, A
56	8	1.0	1577	4	US-10-741-849-7164	Sequence 7164, A
57	8	1.0	2903	5	US-10-282-122A-69069	Sequence 69069, A
58	8	1.0	2903	5	US-10-732-923-13991	Sequence 13991, A
59	7	0.9	23	5	US-10-776-224-147	Sequence 147, A
60	7	0.9	32	4	US-10-425-115-275165	Sequence 275165, A
61	7	0.9	47	4	US-10-425-115-352701	Sequence 352701, A
62	7	0.9	50	3	US-09-864-761-40065	Sequence 40065, A
63	7	0.9	52	4	US-10-425-115-215004	Sequence 215004, A
64	7	0.9	55	4	US-10-767-701-50935	Sequence 50935, A
65	7	0.9	56	4	US-10-425-115-341846	Sequence 341846, A
66	7	0.9	58	4	US-10-117-604-10	Sequence 10, Appl
67	7	0.9	62	4	US-10-425-115-196424	Sequence 196424, A
68	7	0.9	64	4	US-10-424-599-144303	Sequence 144303, A
69	7	0.9	64	4	US-10-424-599-203518	Sequence 203518, A
70	7	0.9	64	4	US-10-767-701-53260	Sequence 53260, A
71	7	0.9	66	4	US-10-424-599-248374	Sequence 248374, A
72	7	0.9	68	4	US-10-424-599-190349	Sequence 190349, A
73	7	0.9	69	4	US-10-425-115-359285	Sequence 359285, A
74	7	0.9	71	4	US-10-424-599-249223	Sequence 249223, A
75	7	0.9	76	4	US-10-282-122A-43360	Sequence 43360, A
76	7	0.9	76	4	US-10-425-115-246828	Sequence 246828, A
77	7	0.9	78	4	US-10-424-599-189046	Sequence 189046, A
78	7	0.9	79	4	US-10-437-963-104699	Sequence 104699, A
79	7	0.9	80	4	US-10-437-963-156781	Sequence 156781, A
80	7	0.9	82	3	US-09-864-408A-4096	Sequence 4096, A
81	7	0.9	83	4	US-10-424-599-188471	Sequence 188471, A
82	7	0.9	84	4	US-10-425-115-219581	Sequence 219581, A
83	7	0.9	85	4	US-10-369-493-21140	Sequence 21140, A
84	7	0.9	87	3	US-09-764-860-347	Sequence 347, A
85	7	0.9	87	4	US-10-074-095-347	Sequence 347, A
86	7	0.9	88	4	US-10-212-872-347	Sequence 347, A
87	7	0.9	88	4	US-10-012-542-325	Sequence 325, A
88	7	0.9	88	4	US-10-115-123-325	Sequence 325, A
89	7	0.9	88	4	US-10-800-834-325	Sequence 325, A
90	7	0.9	88	4	US-10-425-115-364770	Sequence 364770, A
91	7	0.9	90	4	US-10-424-599-174289	Sequence 174289, A
92	7	0.9	92	4	US-10-437-963-188438	Sequence 188438, A
93	7	0.9	93	4	US-10-424-599-146654	Sequence 146654, A
94	7	0.9	96	4	US-10-437-963-123593	Sequence 123593, A
95	7	0.9	101	4	US-10-425-115-258624	Sequence 258624, A
96	7	0.9	102	4	US-10-424-599-259323	Sequence 259323, A
97	7	0.9	105	4	US-10-424-599-227387	Sequence 227387, A
98	7	0.9	106	4	US-10-425-115-338480	Sequence 338480, A
99	7	0.9	107	4	US-10-425-115-354503	Sequence 354503, A
100	7	0.9	110	4	US-10-291-851-93	Sequence 93, Appl

101	7	0.9	113	4	US-10-425-115-258019	Sequence 258019, A	174	7	0.9	310	4	US-10-369-493-12686	Sequence 12686, A
102	7	0.9	122	4	US-10-424-599-168965	Sequence 168965, A	175	7	0.9	315	4	US-10-106-698-5557	Sequence 5557, Ap
103	7	0.9	122	4	US-10-424-599-256379	Sequence 256379, A	176	7	0.9	324	3	US-09-815-242-13895	Sequence 13895, A
104	7	0.9	122	4	US-10-425-115-347287	Sequence 347287, A	177	7	0.9	324	4	US-10-282-122A-76321	Sequence 76321, A
105	7	0.9	122	5	US-10-739-930-8036	Sequence 8036, Ap	178	7	0.9	325	3	US-09-738-626-4841	Sequence 4841, Ap
106	7	0.9	123	4	US-10-425-115-235907	Sequence 235907, A	179	7	0.9	325	4	US-10-781-014-776	Sequence 776, App
107	7	0.9	123	4	US-10-425-115-314619	Sequence 314619, A	180	7	0.9	327	4	US-10-264-237-1918	Sequence 1918, Ap
108	7	0.9	125	4	US-10-767-701-32380	Sequence 32380, A	181	7	0.9	329	4	US-10-012-819-60	Sequence 60, Appl
109	7	0.9	126	4	US-10-437-963-104429	Sequence 104429, A	182	7	0.9	335	3	US-09-934-455-226	Sequence 226, App
110	7	0.9	129	4	US-11-097-143-34038	Sequence 34038, A	183	7	0.9	335	4	US-10-225-066A-834	Sequence 834, App
111	7	0.9	132	4	US-10-276-774-1607	Sequence 1607, Ap	184	7	0.9	335	4	US-10-374-780A-294	Sequence 294, App
112	7	0.9	133	4	US-10-425-115-239682	Sequence 239682, A	185	7	0.9	335	5	US-10-225-066A-834	Sequence 834, App
113	7	0.9	145	4	US-10-425-115-366479	Sequence 366479, A	186	7	0.9	336	4	US-10-146-733-20	Sequence 20, Appl
114	7	0.9	150	4	US-10-282-122A-54511	Sequence 54511, A	187	7	0.9	337	4	US-10-264-237-2731	Sequence 2731, Ap
115	7	0.9	150	4	US-10-767-701-54531	Sequence 54531, A	188	7	0.9	337	4	US-10-282-122A-74662	Sequence 74662, A
116	7	0.9	150	4	US-10-425-115-187306	Sequence 187306, A	189	7	0.9	340	4	US-10-767-701-41329	Sequence 41329, A
117	7	0.9	150	4	US-10-425-115-331739	Sequence 331739, A	190	7	0.9	341	5	US-10-450-763-47487	Sequence 47487, A
118	7	0.9	151	4	US-10-424-599-171238	Sequence 171238, A	191	7	0.9	341	6	US-11-097-143-21942	Sequence 21942, A
119	7	0.9	154	4	US-10-425-115-331169	Sequence 331169, A	192	7	0.9	342	4	US-10-381-898-9	Sequence 9, Appli
120	7	0.9	157	4	US-10-424-599-257335	Sequence 257335, A	193	7	0.9	349	4	US-10-282-122A-51887	Sequence 51887, A
121	7	0.9	169	4	US-10-437-963-125771	Sequence 125771, A	194	7	0.9	351	4	US-10-369-493-3808	Sequence 3808, Ap
122	7	0.9	171	5	US-10-472-928-2480	Sequence 2480, Ap	195	7	0.9	353	4	US-10-425-115-271431	Sequence 271431, A
123	7	0.9	176	4	US-10-425-114-49034	Sequence 49034, A	196	7	0.9	355	4	US-10-357-521-4	Sequence 4, Appli
124	7	0.9	176	5	US-10-732-923-5057	Sequence 5057, Ap	197	7	0.9	355	5	US-10-915-029-8	Sequence 8, Appli
125	7	0.9	177	4	US-10-633-680-76	Sequence 76, Appl	198	7	0.9	356	4	US-10-282-122A-52244	Sequence 52244, A
126	7	0.9	177	4	US-10-632-983-55	Sequence 55, Appl	199	7	0.9	359	4	US-10-225-486-54	Sequence 54, Appl
127	7	0.9	178	3	US-09-798-889-76	Sequence 76, Appl	200	7	0.9	366	4	US-10-369-493-1018	Sequence 1018, Ap
128	7	0.9	182	4	US-10-767-701-52318	Sequence 52318, A	201	7	0.9	381	4	US-10-633-680-49	Sequence 49, Appl
129	7	0.9	186	5	US-10-739-930-8997	Sequence 8997, Ap	202	7	0.9	382	3	US-09-798-889-49	Sequence 49, Appl
130	7	0.9	189	5	US-10-450-763-53433	Sequence 53433, A	203	7	0.9	383	3	US-09-738-626-4870	Sequence 4870, Ap
131	7	0.9	191	4	US-10-437-963-133805	Sequence 133805, A	204	7	0.9	384	5	US-10-732-923-2861	Sequence 2861, Ap
132	7	0.9	194	4	US-10-424-599-173855	Sequence 173855, A	205	7	0.9	386	4	US-10-369-493-8726	Sequence 8726, Ap
133	7	0.9	197	4	US-10-425-114-42546	Sequence 42546, A	206	7	0.9	386	5	US-10-450-763-51472	Sequence 51472, A
134	7	0.9	199	4	US-10-424-599-192625	Sequence 192625, A	207	7	0.9	390	4	US-10-282-122A-48185	Sequence 48185, A
135	7	0.9	199	4	US-10-767-701-46512	Sequence 46512, A	208	7	0.9	391	4	US-10-437-963-189621	Sequence 189621, A
136	7	0.9	200	4	US-10-425-115-279847	Sequence 279847, A	209	7	0.9	398	4	US-10-425-114-71531	Sequence 71531, A
137	7	0.9	208	6	US-11-097-143-32487	Sequence 32487, A	210	7	0.9	401	4	US-10-424-599-269452	Sequence 269452, A
138	7	0.9	213	4	US-10-029-386-34063	Sequence 34063, A	211	7	0.9	405	4	US-10-369-493-8649	Sequence 8649, Ap
139	7	0.9	213	4	US-10-425-115-185030	Sequence 185030, A	212	7	0.9	405	4	US-10-369-493-20689	Sequence 20689, A
140	7	0.9	217	4	US-10-425-114-39820	Sequence 39820, A	213	7	0.9	405	4	US-10-425-115-192417	Sequence 192417, A
141	7	0.9	220	4	US-10-437-963-187087	Sequence 187087, A	214	7	0.9	411	4	US-10-369-493-12939	Sequence 12939, A
142	7	0.9	221	4	US-10-369-493-8397	Sequence 8397, Ap	215	7	0.9	416	4	US-10-282-122A-70224	Sequence 70224, A
143	7	0.9	221	4	US-10-425-115-337161	Sequence 337161, A	216	7	0.9	417	5	US-10-450-763-33693	Sequence 33693, A
144	7	0.9	226	6	US-11-097-143-30105	Sequence 30105, A	217	7	0.9	423	5	US-10-450-763-58445	Sequence 58445, A
145	7	0.9	228	4	US-10-369-493-20929	Sequence 20929, A	218	7	0.9	425	4	US-10-117-018-8	Sequence 8, Appli
146	7	0.9	228	4	US-10-424-599-171239	Sequence 171239, A	219	7	0.9	426	5	US-10-946-424-8	Sequence 8, Appli
147	7	0.9	234	3	US-09-882-227-24	Sequence 24, Appl	220	7	0.9	426	4	US-10-369-493-4635	Sequence 4635, Ap
148	7	0.9	234	4	US-10-335-977-8510	Sequence 8510, Ap	221	7	0.9	426	4	US-10-425-115-368617	Sequence 368617, A
149	7	0.9	234	4	US-10-425-115-185029	Sequence 185029, A	222	7	0.9	426	5	US-10-732-923-10735	Sequence 10735, A
150	7	0.9	243	5	US-10-450-763-54612	Sequence 54612, A	223	7	0.9	429	4	US-10-282-122A-51466	Sequence 51466, A
151	7	0.9	245	4	US-10-425-115-351748	Sequence 351748, A	224	7	0.9	432	4	US-10-437-963-182668	Sequence 182668, A
152	7	0.9	250	6	US-11-097-143-5376	Sequence 5376, Ap	225	7	0.9	433	4	US-10-282-122A-49892	Sequence 49892, A
153	7	0.9	254	4	US-10-395-607-127	Sequence 127, App	226	7	0.9	434	3	US-10-369-493-7393	Sequence 7393, Ap
154	7	0.9	254	4	US-10-799-870-127	Sequence 127, App	227	7	0.9	442	3	US-09-866-050A-641	Sequence 641, App
155	7	0.9	255	5	US-10-472-928-4076	Sequence 4076, Ap	228	7	0.9	444	4	US-10-369-493-6911	Sequence 6911, Ap
156	7	0.9	260	4	US-10-425-115-249662	Sequence 249662, A	229	7	0.9	444	5	US-10-650-467-42	Sequence 42, Appl
157	7	0.9	262	4	US-10-424-599-232524	Sequence 232524, A	230	7	0.9	444	5	US-10-450-763-38749	Sequence 38749, A
158	7	0.9	263	4	US-10-424-599-189044	Sequence 189044, A	231	7	0.9	445	4	US-10-369-493-4105	Sequence 4105, Ap
159	7	0.9	272	4	US-10-437-963-201475	Sequence 201475, A	232	7	0.9	456	4	US-10-369-493-20284	Sequence 20284, A
160	7	0.9	273	4	US-10-437-963-127798	Sequence 127798, A	233	7	0.9	458	3	US-09-972-268-21	Sequence 21, Appl
161	7	0.9	274	4	US-10-437-963-116008	Sequence 116008, A	234	7	0.9	458	4	US-10-299-636-99	Sequence 99, Appl
162	7	0.9	280	4	US-10-282-122A-74821	Sequence 74821, A	235	7	0.9	459	4	US-10-282-122A-70133	Sequence 70133, A
163	7	0.9	282	4	US-10-094-749-2096	Sequence 2096, Ap	236	7	0.9	464	3	US-09-912-020-281	Sequence 281, App
164	7	0.9	285	4	US-10-282-122A-72956	Sequence 72956, A	237	7	0.9	464	4	US-10-287-270-441	Sequence 441, App
165	7	0.9	288	4	US-10-369-493-22433	Sequence 22433, A	238	7	0.9	464	5	US-10-282-122A-42613	Sequence 42613, A
166	7	0.9	290	4	US-10-276-774-1357	Sequence 1357, Ap	239	7	0.9	464	5	US-10-771-241-281	Sequence 281, App
167	7	0.9	292	4	US-10-282-122A-57001	Sequence 57001, A	240	7	0.9	465	5	US-10-904-588-18	Sequence 18, Appl
168	7	0.9	293	4	US-10-369-493-13324	Sequence 13324, A	241	7	0.9	469	4	US-10-369-493-13381	Sequence 13381, A
169	7	0.9	301	4	US-10-156-761-13367	Sequence 13367, A	242	7	0.9	472	3	US-09-870-162A-3	Sequence 3, Appli
170	7	0.9	305	4	US-10-369-493-640	Sequence 640, App	243	7	0.9	478	5	US-10-469-204-141	Sequence 141, App
171	7	0.9	307	4	US-10-424-599-224191	Sequence 224191, A	244	7	0.9	478	6	US-11-097-143-25683	Sequence 25683, A
172	7	0.9	308	4	US-10-156-761-14268	Sequence 14268, A	245	7	0.9	488	4	US-10-437-963-180174	Sequence 180174, A
173	7	0.9	308	5	US-10-732-923-10057	Sequence 10057, A	246	7	0.9	490	4	US-10-074-152-26	Sequence 26, Appl



247	7	0.9	497	3	US-09-815-242-13344	Sequence 13344, A	320	7	0.9	717	4	US-10-267-502-250	Sequence 250, App
248	7	0.9	497	4	US-10-282-122A-73912	Sequence 73912, A	321	7	0.9	717	6	US-11-097-143-11619	Sequence 11619, A
249	7	0.9	497	5	US-10-472-928-1718	Sequence 1718, Ap	322	7	0.9	732	4	US-10-184-644-577	Sequence 577, App
250	7	0.9	504	5	US-10-617-320-3732	Sequence 3732, Ap	323	7	0.9	732	4	US-10-184-634-577	Sequence 577, App
251	7	0.9	510	5	US-10-732-923-13923	Sequence 13923, A	324	7	0.9	732	4	US-10-282-122A-70070	Sequence 70070, A
252	7	0.9	514	4	US-10-161-572-60	Sequence 60, Appl	325	7	0.9	755	4	US-10-437-963-171603	Sequence 171603, A
253	7	0.9	517	3	US-09-972-268-20	Sequence 20, Appl	326	7	0.9	761	4	US-10-416-330-35	Sequence 35, Appl
254	7	0.9	518	3	US-09-915-172-20	Sequence 20, Appl	327	7	0.9	786	5	US-10-874-049-3	Sequence 3, Appl
255	7	0.9	518	4	US-10-369-493-18702	Sequence 18702, A	328	7	0.9	789	5	US-10-874-049-5	Sequence 5, Appl
256	7	0.9	518	5	US-10-752-986-20	Sequence 20, Appl	329	7	0.9	792	4	US-10-087-192-1977	Sequence 1977, Ap
257	7	0.9	521	4	US-10-282-122A-63634	Sequence 63634, A	330	7	0.9	792	5	US-10-450-763-46062	Sequence 46062, A
258	7	0.9	522	4	US-10-282-122A-50014	Sequence 50014, A	331	7	0.9	797	4	US-10-369-493-12480	Sequence 12480, A
259	7	0.9	527	4	US-10-282-122A-47475	Sequence 47475, A	332	7	0.9	818	3	US-09-738-626-6491	Sequence 6491, Ap
260	7	0.9	528	6	US-11-097-143-41799	Sequence 41799, A	333	7	0.9	822	4	US-10-437-963-104983	Sequence 104983, A
261	7	0.9	529	3	US-09-954-314-22	Sequence 22, Appl	334	7	0.9	823	6	US-11-097-143-41244	Sequence 41244, A
262	7	0.9	529	4	US-10-230-562-22	Sequence 22, Appl	335	7	0.9	850	4	US-10-238-075-1021	Sequence 1021, Ap
263	7	0.9	529	5	US-10-230-026-16	Sequence 16, Appl	336	7	0.9	874	4	US-10-282-122A-61488	Sequence 61488, A
264	7	0.9	529	5	US-10-739-930-9550	Sequence 9550, Ap	337	7	0.9	897	6	US-10-087-143-13575	Sequence 13575, A
265	7	0.9	529	5	US-10-486-307-16	Sequence 16, Appl	338	7	0.9	902	4	US-10-184-644-303	Sequence 303, App
266	7	0.9	539	4	US-10-424-599-227399	Sequence 227399, A	339	7	0.9	902	4	US-10-184-634-303	Sequence 303, App
267	7	0.9	545	5	US-10-287-436A-271	Sequence 271, App	340	7	0.9	902	4	US-10-063-685-93	Sequence 93, Appl
268	7	0.9	546	5	US-10-287-436A-212	Sequence 212, App	341	7	0.9	914	5	US-10-484-703-35	Sequence 35, Appl
269	7	0.9	562	6	US-11-097-143-21426	Sequence 21426, A	342	7	0.9	933	4	US-10-087-192-1980	Sequence 1980, Ap
270	7	0.9	564	5	US-10-739-930-9713	Sequence 9713, Ap	343	7	0.9	953	3	US-09-884-696-3	Sequence 3, Appl
271	7	0.9	564	5	US-10-481-113-28	Sequence 28, Appl	344	7	0.9	953	3	US-10-148-884-5	Sequence 5, Appl
272	7	0.9	568	4	US-10-032-585-7920	Sequence 7920, Ap	345	7	0.9	956	5	US-10-425-115-337013	Sequence 337013, A
273	7	0.9	572	4	US-10-437-963-173191	Sequence 173191, A	346	7	0.9	959	4	US-10-080-608A-20	Sequence 20, Appl
274	7	0.9	572	5	US-10-481-113-104	Sequence 104, App	347	7	0.9	963	4	US-10-370-685-109	Sequence 109, App
275	7	0.9	572	5	US-10-481-032A-66	Sequence 66, Appl	348	7	0.9	963	4	US-10-370-685-111	Sequence 111, App
276	7	0.9	573	6	US-11-097-143-8811	Sequence 8811, Ap	349	7	0.9	963	4	US-11-009-554-10	Sequence 10, Appl
277	7	0.9	578	4	US-10-425-115-249810	Sequence 249810, A	350	7	0.9	967	6	US-10-478-245-9	Sequence 9, Appl
278	7	0.9	578	5	US-10-450-763-54609	Sequence 54609, A	351	7	0.9	969	4	US-10-108-360A-4153	Sequence 4153, Ap
279	7	0.9	580	4	US-10-647-057-4	Sequence 4, Appl	352	7	0.9	978	4	US-10-425-115-194052	Sequence 194052, A
280	7	0.9	581	4	US-10-767-701-46924	Sequence 46924, A	353	7	0.9	992	4	US-09-738-626-4363	Sequence 4363, Ap
281	7	0.9	584	4	US-10-282-122A-47689	Sequence 47689, A	354	7	0.9	1016	4	US-10-282-122A-69491	Sequence 69491, A
282	7	0.9	587	3	US-09-893-519A-42	Sequence 42, Appl	355	7	0.9	1019	4	US-10-408-765A-1661	Sequence 1661, Ap
283	7	0.9	589	4	US-10-205-194-144	Sequence 144, App	356	7	0.9	1031	4	US-10-437-963-169433	Sequence 169433, A
284	7	0.9	589	4	US-10-437-963-127286	Sequence 127286, A	357	7	0.9	1031	4	US-10-001-885-108	Sequence 108, App
285	7	0.9	590	5	US-10-831-070-10	Sequence 10, Appl	358	7	0.9	1054	6	US-11-057-447-108	Sequence 108, App
286	7	0.9	604	3	US-09-862-027-17	Sequence 17, Appl	359	7	0.9	1054	6	US-11-097-143-11583	Sequence 11583, A
287	7	0.9	619	4	US-10-989-228-17	Sequence 17, Appl	360	7	0.9	1078	6	US-10-335-977-5265	Sequence 5265, Ap
288	7	0.9	619	4	US-10-369-493-5855	Sequence 5855, Ap	361	7	0.9	1120	4	US-10-437-963-152821	Sequence 152821, A
289	7	0.9	620	3	US-09-893-519A-59	Sequence 59, Appl	362	7	0.9	1121	2	US-08-915-048A-2	Sequence 2, Appl
290	7	0.9	620	4	US-10-369-493-1442	Sequence 1442, Ap	363	7	0.9	1136	5	US-10-484-703-36	Sequence 36, Appl
291	7	0.9	622	4	US-10-197-666A-22	Sequence 22, Appl	364	7	0.9	1139	4	US-10-467-535-11	Sequence 11, Appl
292	7	0.9	622	4	US-10-024-298A-63	Sequence 63, Appl	365	7	0.9	1161	4	US-10-467-535-5	Sequence 5, Appl
293	7	0.9	622	4	US-10-042-211A-63	Sequence 63, Appl	366	7	0.9	1174	4	US-10-184-644-353	Sequence 353, App
294	7	0.9	622	4	US-10-617-217A-63	Sequence 63, Appl	367	7	0.9	1174	4	US-10-184-634-353	Sequence 34, Appl
295	7	0.9	622	4	US-10-024-298A-63	Sequence 63, Appl	368	7	0.9	1178	5	US-10-484-703-34	Sequence 1202, Ap
296	7	0.9	625	4	US-10-369-493-22882	Sequence 22882, A	369	7	0.9	1187	4	US-10-389-566-1202	Sequence 188299, A
297	7	0.9	627	5	US-10-450-763-48621	Sequence 48621, A	370	7	0.9	1248	4	US-10-437-963-188299	Sequence 1, Appl
298	7	0.9	628	4	US-10-156-761-10990	Sequence 10990, A	371	7	0.9	1264	4	US-10-123-155-1	Sequence 1, Appl
299	7	0.9	628	5	US-10-450-763-54036	Sequence 54036, A	372	7	0.9	1264	4	US-10-146-731-1	Sequence 1, Appl
300	7	0.9	632	4	US-10-024-298A-65	Sequence 65, Appl	373	7	0.9	1264	4	US-10-140-923-1	Sequence 1, Appl
301	7	0.9	632	4	US-10-042-211A-65	Sequence 65, Appl	374	7	0.9	1264	4	US-10-141-761-1	Sequence 1, Appl
302	7	0.9	632	4	US-10-617-217A-65	Sequence 65, Appl	375	7	0.9	1264	4	US-10-142-885-1	Sequence 1, Appl
303	7	0.9	632	4	US-10-024-298A-65	Sequence 65, Appl	376	7	0.9	1264	4	US-10-158-790-1	Sequence 1, Appl
304	7	0.9	640	6	US-11-097-143-317987	Sequence 317987, A	377	7	0.9	1264	4	US-10-137-871-1	Sequence 1, Appl
305	7	0.9	649	6	US-10-425-115-317987	Sequence 10503, A	378	7	0.9	1264	4	US-10-137-871-1	Sequence 1, Appl
306	7	0.9	663	4	US-10-282-122A-52415	Sequence 52415, A	379	7	0.9	1264	4	US-10-140-923-1	Sequence 1, Appl
307	7	0.9	666	3	US-09-746-660A-46	Sequence 46, Appl	380	7	0.9	1264	4	US-10-141-759-1	Sequence 1, Appl
308	7	0.9	667	5	US-10-767-701-46248	Sequence 46248, A	381	7	0.9	1264	4	US-10-140-805-1	Sequence 1, Appl
309	7	0.9	667	5	US-10-450-763-47260	Sequence 47260, A	382	7	0.9	1264	4	US-10-140-864-1	Sequence 1, Appl
310	7	0.9	673	4	US-10-433-794-2	Sequence 2, Appl	383	7	0.9	1264	4	US-11-097-143-10734	Sequence 10734, A
311	7	0.9	676	5	US-10-617-320-4098	Sequence 4098, Ap	384	7	0.9	1268	6	US-10-302-279-60	Sequence 60, Appl
312	7	0.9	684	4	US-10-437-963-111247	Sequence 111247, A	385	7	0.9	1296	4	US-10-184-644-599	Sequence 599, App
313	7	0.9	686	4	US-10-282-122A-67777	Sequence 67777, A	386	7	0.9	1297	4	US-10-184-634-599	Sequence 599, App
314	7	0.9	692	4	US-10-369-493-8800	Sequence 8800, Ap	387	7	0.9	1297	4	US-10-123-155-435	Sequence 435, App
315	7	0.9	695	3	US-09-305-924-13	Sequence 13, Appl	388	7	0.9	1297	4	US-10-146-731-435	Sequence 435, App
316	7	0.9	709	4	US-10-156-761-12338	Sequence 12338, A	389	7	0.9	1297	4	US-10-140-472-435	Sequence 435, App
317	7	0.9	709	4	US-10-425-114-46512	Sequence 46512, A	390	7	0.9	1297	4	US-10-141-761-435	Sequence 435, App
318	7	0.9	711	4	US-10-425-114-54901	Sequence 54901, A	391	7	0.9	1297	4	US-10-141-761-435	Sequence 435, App
319	7	0.9	711	4	US-10-425-115-317988	Sequence 317988, A	392	7	0.9	1297	4		

393	7	0.9	1297	4	US-10-142-885-435	Sequence 435, App	466	7	0.9	1484	4	US-10-141-761-447	Sequence 447, App
394	7	0.9	1297	4	US-10-158-790-435	Sequence 435, App	467	7	0.9	1484	4	US-10-142-885-447	Sequence 447, App
395	7	0.9	1297	4	US-10-137-871-435	Sequence 435, App	468	7	0.9	1484	4	US-10-158-790-447	Sequence 447, App
396	7	0.9	1297	4	US-10-140-923-435	Sequence 435, App	469	7	0.9	1484	4	US-10-137-871-447	Sequence 447, App
397	7	0.9	1297	4	US-10-141-756-435	Sequence 435, App	470	7	0.9	1484	4	US-10-140-923-447	Sequence 447, App
398	7	0.9	1297	4	US-10-141-756-435	Sequence 435, App	471	7	0.9	1484	4	US-10-141-756-447	Sequence 447, App
399	7	0.9	1297	4	US-10-140-805-435	Sequence 435, App	472	7	0.9	1484	4	US-10-141-759-447	Sequence 447, App
400	7	0.9	1297	4	US-10-140-805-435	Sequence 435, App	473	7	0.9	1484	4	US-10-140-805-447	Sequence 447, App
401	7	0.9	1320	4	US-10-161-051-167	Sequence 167, App	474	7	0.9	1484	4	US-10-140-864-447	Sequence 447, App
402	7	0.9	1334	4	US-10-184-644-339	Sequence 339, App	475	7	0.9	1515	4	US-10-184-644-399	Sequence 399, App
403	7	0.9	1334	4	US-10-184-634-339	Sequence 339, App	476	7	0.9	1515	4	US-10-184-634-399	Sequence 399, App
404	7	0.9	1336	4	US-10-224-999A-3482	Sequence 3482, Ap	477	7	0.9	1515	4	US-10-063-685-157	Sequence 157, App
405	7	0.9	1336	4	US-10-437-963-110486	Sequence 110486,	478	7	0.9	1536	4	US-10-184-644-461	Sequence 461, App
406	7	0.9	1376	4	US-10-123-155-161	Sequence 161, App	479	7	0.9	1536	4	US-10-184-634-461	Sequence 461, App
407	7	0.9	1376	4	US-10-146-731-161	Sequence 161, App	480	7	0.9	1576	4	US-10-335-977-5266	Sequence 5266, Ap
408	7	0.9	1376	4	US-10-140-472-161	Sequence 161, App	481	7	0.9	1584	5	US-10-732-923-12885	Sequence 12885, A
409	7	0.9	1376	4	US-10-141-761-161	Sequence 161, App	482	7	0.9	1624	4	US-10-123-155-181	Sequence 181, App
410	7	0.9	1376	4	US-10-142-885-161	Sequence 161, App	483	7	0.9	1624	4	US-10-146-731-181	Sequence 181, App
411	7	0.9	1376	4	US-10-158-790-161	Sequence 161, App	484	7	0.9	1624	4	US-10-140-472-181	Sequence 181, App
412	7	0.9	1376	4	US-10-137-871-161	Sequence 161, App	485	7	0.9	1624	4	US-10-141-761-181	Sequence 181, App
413	7	0.9	1376	4	US-10-140-923-161	Sequence 161, App	486	7	0.9	1624	4	US-10-142-885-181	Sequence 181, App
414	7	0.9	1376	4	US-10-141-756-161	Sequence 161, App	487	7	0.9	1624	4	US-10-158-790-181	Sequence 181, App
415	7	0.9	1376	4	US-10-141-759-161	Sequence 161, App	488	7	0.9	1624	4	US-10-137-871-181	Sequence 181, App
416	7	0.9	1376	4	US-10-140-805-161	Sequence 161, App	489	7	0.9	1624	4	US-10-140-923-181	Sequence 181, App
417	7	0.9	1376	4	US-10-140-864-161	Sequence 161, App	490	7	0.9	1624	4	US-10-141-756-181	Sequence 181, App
418	7	0.9	1390	4	US-10-137-418A-2	Sequence 2, Appli	491	7	0.9	1624	4	US-10-141-759-181	Sequence 181, App
419	7	0.9	1419	4	US-10-123-155-517	Sequence 517, App	492	7	0.9	1624	4	US-10-140-805-181	Sequence 181, App
420	7	0.9	1419	4	US-10-146-731-517	Sequence 517, App	493	7	0.9	1624	4	US-10-140-864-181	Sequence 181, App
421	7	0.9	1419	4	US-10-140-923-517	Sequence 517, App	494	7	0.9	1628	5	US-10-450-763-32554	Sequence 32554, A
422	7	0.9	1419	4	US-10-141-761-517	Sequence 517, App	495	7	0.9	1665	4	US-10-184-644-285	Sequence 285, App
423	7	0.9	1419	4	US-10-142-885-517	Sequence 517, App	496	7	0.9	1665	4	US-10-184-634-285	Sequence 285, App
424	7	0.9	1419	4	US-10-158-790-517	Sequence 517, App	497	7	0.9	1665	4	US-10-063-685-85	Sequence 85, Appli
425	7	0.9	1419	4	US-10-137-871-517	Sequence 517, App	498	7	0.9	1686	4	US-10-092-219-2	Sequence 2, Appli
426	7	0.9	1419	4	US-10-140-923-517	Sequence 517, App	499	7	0.9	1730	4	US-10-123-155-7	Sequence 7, Appli
427	7	0.9	1419	4	US-10-141-756-517	Sequence 517, App	500	7	0.9	1730	4	US-10-146-731-7	Sequence 7, Appli
428	7	0.9	1419	4	US-10-141-759-517	Sequence 517, App	501	7	0.9	1730	4	US-10-140-472-7	Sequence 7, Appli
429	7	0.9	1419	4	US-10-140-805-517	Sequence 517, App	502	7	0.9	1730	4	US-10-141-761-7	Sequence 7, Appli
430	7	0.9	1419	4	US-10-140-864-517	Sequence 517, App	503	7	0.9	1730	4	US-10-142-885-7	Sequence 7, Appli
431	7	0.9	1419	4	US-10-092-900A-82	Sequence 82, Appl	504	7	0.9	1730	4	US-10-158-790-7	Sequence 7, Appli
432	7	0.9	1423	4	US-10-092-900A-86	Sequence 86, Appl	505	7	0.9	1730	4	US-10-137-871-7	Sequence 7, Appli
433	7	0.9	1434	2	US-08-954-701A-10	Sequence 10, Appl	506	7	0.9	1730	4	US-10-140-923-7	Sequence 7, Appli
434	7	0.9	1434	2	US-09-754-032-10	Sequence 10, Appl	507	7	0.9	1730	4	US-10-141-756-7	Sequence 7, Appli
435	7	0.9	1434	4	US-10-421-446-10	Sequence 10, Appl	508	7	0.9	1730	4	US-10-141-759-7	Sequence 7, Appli
436	7	0.9	1439	4	US-10-220-481-73	Sequence 73, Appl	509	7	0.9	1730	4	US-10-140-805-7	Sequence 7, Appli
437	7	0.9	1447	2	US-08-954-701A-19	Sequence 19, Appl	510	7	0.9	1771	4	US-10-140-864-7	Sequence 7, Appli
438	7	0.9	1447	3	US-09-898-533-5	Sequence 5, Appli	511	7	0.9	1771	4	US-10-184-634-17	Sequence 17, Appl
439	7	0.9	1447	3	US-09-754-032-19	Sequence 19, Appl	512	7	0.9	1771	4	US-10-184-634-17	Sequence 17, Appl
440	7	0.9	1447	4	US-10-421-446-19	Sequence 19, Appl	513	7	0.9	1775	4	US-10-335-977-5267	Sequence 5267, Ap
441	7	0.9	1447	4	US-10-731-844-6	Sequence 6, Appli	514	7	0.9	1808	4	US-10-123-155-47	Sequence 47, Appl
442	7	0.9	1447	4	US-10-282-122A-65711	Sequence 65711, A	515	7	0.9	1808	4	US-10-146-731-47	Sequence 47, Appl
443	7	0.9	1454	4	US-10-742-345-2	Sequence 2, Appli	516	7	0.9	1808	4	US-10-140-472-47	Sequence 47, Appl
444	7	0.9	1455	5	US-10-484-703-32	Sequence 32, Appl	517	7	0.9	1808	4	US-10-141-761-47	Sequence 47, Appl
445	7	0.9	1457	4	US-10-220-481-71	Sequence 71, Appl	518	7	0.9	1808	4	US-10-142-885-47	Sequence 47, Appl
446	7	0.9	1457	4	US-10-742-345-4	Sequence 4, Appli	519	7	0.9	1808	4	US-10-158-790-47	Sequence 47, Appl
447	7	0.9	1457	5	US-10-915-740A-1047	Sequence 1047, Ap	520	7	0.9	1808	4	US-10-137-871-47	Sequence 47, Appl
448	7	0.9	1458	4	US-10-054-691-2	Sequence 2, Appli	521	7	0.9	1808	4	US-10-140-923-47	Sequence 47, Appl
449	7	0.9	1458	4	US-10-478-245-1	Sequence 1, Appli	522	7	0.9	1808	4	US-10-141-756-47	Sequence 47, Appl
450	7	0.9	1468	4	US-10-282-122A-65027	Sequence 65027, A	523	7	0.9	1808	4	US-10-141-759-47	Sequence 47, Appl
451	7	0.9	1471	4	US-10-123-155-281	Sequence 281, App	524	7	0.9	1808	4	US-10-140-805-47	Sequence 47, Appl
452	7	0.9	1471	4	US-10-146-731-281	Sequence 281, App	525	7	0.9	1808	4	US-10-140-864-47	Sequence 47, Appl
453	7	0.9	1471	4	US-10-140-472-281	Sequence 281, App	526	7	0.9	1849	4	US-10-184-644-133	Sequence 133, App
454	7	0.9	1471	4	US-10-141-761-281	Sequence 281, App	527	7	0.9	1849	4	US-10-184-634-133	Sequence 133, App
455	7	0.9	1471	4	US-10-142-885-281	Sequence 281, App	528	7	0.9	1849	4	US-10-063-685-21	Sequence 21, Appl
456	7	0.9	1471	4	US-10-158-790-281	Sequence 281, App	529	7	0.9	1883	4	US-10-123-155-501	Sequence 501, App
457	7	0.9	1471	4	US-10-137-871-281	Sequence 281, App	530	7	0.9	1883	4	US-10-146-731-501	Sequence 501, App
458	7	0.9	1471	4	US-10-140-923-281	Sequence 281, App	531	7	0.9	1883	4	US-10-140-472-501	Sequence 501, App
459	7	0.9	1471	4	US-10-141-756-281	Sequence 281, App	532	7	0.9	1883	4	US-10-141-761-501	Sequence 501, App
460	7	0.9	1471	4	US-10-141-759-281	Sequence 281, App	533	7	0.9	1883	4	US-10-142-885-501	Sequence 501, App
461	7	0.9	1471	4	US-10-140-805-281	Sequence 281, App	534	7	0.9	1883	4	US-10-158-790-501	Sequence 501, App
462	7	0.9	1471	4	US-10-140-864-281	Sequence 281, App	535	7	0.9	1883	4	US-10-137-871-501	Sequence 501, App
463	7	0.9	1484	4	US-10-123-155-447	Sequence 447, App	536	7	0.9	1883	4	US-10-140-923-501	Sequence 501, App
464	7	0.9	1484	4	US-10-146-731-447	Sequence 447, App	537	7	0.9	1883	4	US-10-141-756-501	Sequence 501, App
465	7	0.9	1484	4	US-10-140-472-447	Sequence 447, App	538	7	0.9	1883	4	US-10-141-759-501	Sequence 501, App

539	7	0.9	1883	4	US-10-140-805-501	Sequence 501, App	612	7	0.9	2457	4	US-10-184-644-569	Sequence 569, App
540	7	0.9	1883	4	US-10-140-864-501	Sequence 501, App	613	7	0.9	2457	4	US-10-184-634-569	Sequence 569, App
541	7	0.9	1912	4	US-10-188-186-48	Sequence 48, Appli	614	7	0.9	2478	4	US-10-184-644-107	Sequence 107, App
542	7	0.9	1943	4	US-10-282-122A-58750	Sequence 58750, A	615	7	0.9	2478	4	US-10-184-634-107	Sequence 107, Appli
543	7	0.9	1974	3	US-09-895-913A-12	Sequence 12, Appl	616	7	0.9	2497	5	US-10-481-582-4	Sequence 4, Appli
544	7	0.9	1975	4	US-10-123-155-105	Sequence 105, App	617	7	0.9	2558	4	US-10-184-644-103	Sequence 103, App
545	7	0.9	1975	4	US-10-146-731-105	Sequence 105, App	618	7	0.9	2558	4	US-10-184-634-103	Sequence 103, App
546	7	0.9	1975	4	US-10-140-472-105	Sequence 105, App	619	7	0.9	2594	4	US-10-123-155-245	Sequence 245, App
547	7	0.9	1975	4	US-10-140-472-105	Sequence 105, App	620	7	0.9	2594	4	US-10-146-731-245	Sequence 245, App
548	7	0.9	1975	4	US-10-141-761-105	Sequence 105, App	621	7	0.9	2594	4	US-10-140-472-245	Sequence 245, App
549	7	0.9	1975	4	US-10-142-885-105	Sequence 105, App	622	7	0.9	2594	4	US-10-141-761-245	Sequence 245, App
550	7	0.9	1975	4	US-10-158-790-105	Sequence 105, App	623	7	0.9	2594	4	US-10-142-885-245	Sequence 245, App
551	7	0.9	1975	4	US-10-137-871-105	Sequence 105, App	624	7	0.9	2594	4	US-10-158-790-245	Sequence 245, App
552	7	0.9	1975	4	US-10-140-923-105	Sequence 105, App	625	7	0.9	2594	4	US-10-137-871-245	Sequence 245, App
553	7	0.9	1975	4	US-10-141-756-105	Sequence 105, App	626	7	0.9	2594	4	US-10-140-923-245	Sequence 245, App
554	7	0.9	1975	4	US-10-141-759-105	Sequence 105, App	627	7	0.9	2594	4	US-10-141-756-245	Sequence 245, App
555	7	0.9	1975	4	US-10-140-864-105	Sequence 105, App	628	7	0.9	2594	4	US-10-141-759-245	Sequence 245, App
556	7	0.9	1984	5	US-10-140-864-105	Sequence 105, App	629	7	0.9	2594	4	US-10-140-805-245	Sequence 245, App
557	7	0.9	2037	4	US-10-450-763-31697	Sequence 31697, A	630	7	0.9	2594	4	US-10-140-864-245	Sequence 245, App
558	7	0.9	2037	4	US-10-184-644-591	Sequence 591, App	631	7	0.9	2598	4	US-10-063-685-151	Sequence 151, App
559	7	0.9	2055	5	US-10-184-634-591	Sequence 591, App	632	7	0.9	2609	4	US-10-184-644-407	Sequence 407, App
560	7	0.9	2103	4	US-10-481-582-3	Sequence 3, Appli	633	7	0.9	2615	4	US-10-184-634-523	Sequence 523, App
561	7	0.9	2103	4	US-10-184-644-319	Sequence 319, App	634	7	0.9	2615	4	US-10-184-644-523	Sequence 523, App
562	7	0.9	2103	4	US-10-184-634-319	Sequence 319, App	635	7	0.9	2615	4	US-10-238-075-1119	Sequence 1119, App
563	7	0.9	2134	4	US-10-063-685-105	Sequence 105, App	636	7	0.9	2819	4	US-10-184-644-109	Sequence 109, App
564	7	0.9	2134	4	US-10-123-155-179	Sequence 179, App	637	7	0.9	2819	4	US-10-184-634-109	Sequence 109, App
565	7	0.9	2134	4	US-10-146-731-179	Sequence 179, App	638	7	0.9	2834	4	US-10-085-959-252	Sequence 252, App
566	7	0.9	2134	4	US-10-140-472-179	Sequence 179, App	639	7	0.9	2916	4	US-10-123-155-69	Sequence 69, Appl
567	7	0.9	2134	4	US-10-141-761-179	Sequence 179, App	640	7	0.9	2916	4	US-10-146-731-69	Sequence 69, Appl
568	7	0.9	2134	4	US-10-142-885-179	Sequence 179, App	641	7	0.9	2916	4	US-10-140-472-69	Sequence 69, Appl
569	7	0.9	2134	4	US-10-158-790-179	Sequence 179, App	642	7	0.9	2916	4	US-10-140-472-69	Sequence 69, Appl
570	7	0.9	2134	4	US-10-137-871-179	Sequence 179, App	643	7	0.9	2916	4	US-10-141-761-69	Sequence 69, Appl
571	7	0.9	2134	4	US-10-140-923-179	Sequence 179, App	644	7	0.9	2916	4	US-10-142-885-69	Sequence 69, Appl
572	7	0.9	2134	4	US-10-141-759-179	Sequence 179, App	645	7	0.9	2916	4	US-10-158-790-69	Sequence 69, Appl
573	7	0.9	2134	4	US-10-140-805-179	Sequence 179, App	646	7	0.9	2916	4	US-10-137-871-69	Sequence 69, Appl
574	7	0.9	2134	4	US-10-140-864-179	Sequence 179, App	647	7	0.9	2916	4	US-10-140-923-69	Sequence 69, Appl
575	7	0.9	2237	4	US-10-123-155-45	Sequence 45, Appl	648	7	0.9	2916	4	US-10-141-756-69	Sequence 69, Appl
576	7	0.9	2237	4	US-10-146-731-45	Sequence 45, Appl	649	7	0.9	2916	4	US-10-141-759-69	Sequence 69, Appl
577	7	0.9	2237	4	US-10-140-472-45	Sequence 45, Appl	650	7	0.9	2916	4	US-10-140-805-69	Sequence 69, Appl
578	7	0.9	2237	4	US-10-141-761-45	Sequence 45, Appl	651	7	0.9	2916	4	US-10-140-864-69	Sequence 69, Appl
579	7	0.9	2237	4	US-10-142-885-45	Sequence 45, Appl	652	7	0.9	2956	4	US-10-184-644-73	Sequence 73, Appl
580	7	0.9	2237	4	US-10-158-790-45	Sequence 45, Appl	653	7	0.9	2956	4	US-10-184-634-73	Sequence 73, Appl
581	7	0.9	2237	4	US-10-137-871-45	Sequence 45, Appl	654	7	0.9	3033	4	US-10-184-644-1	Sequence 1, Appli
582	7	0.9	2237	4	US-10-140-923-45	Sequence 45, Appl	655	7	0.9	3038	4	US-10-184-644-261	Sequence 261, App
583	7	0.9	2237	4	US-10-141-756-45	Sequence 45, Appl	656	7	0.9	3038	4	US-10-184-634-261	Sequence 261, App
584	7	0.9	2237	4	US-10-140-805-45	Sequence 45, Appl	657	7	0.9	3089	4	US-10-184-644-61	Sequence 61, Appl
585	7	0.9	2274	4	US-10-140-864-45	Sequence 45, Appl	658	7	0.9	3089	4	US-10-184-634-61	Sequence 61, Appl
586	7	0.9	2274	4	US-10-267-502-373	Sequence 373, App	659	7	0.9	3122	4	US-10-200-562-201	Sequence 201, App
587	7	0.9	2274	5	US-10-805-684-140	Sequence 140, App	660	7	0.9	3122	4	US-10-237-551-201	Sequence 201, App
588	7	0.9	2275	4	US-10-184-644-401	Sequence 401, App	661	7	0.9	3122	4	US-10-237-551-250	Sequence 250, App
589	7	0.9	2275	4	US-10-184-634-401	Sequence 401, App	662	7	0.9	3122	5	US-10-945-050-201	Sequence 201, App
590	7	0.9	2303	4	US-10-267-502-371	Sequence 371, App	663	7	0.9	3122	5	US-10-945-050-250	Sequence 250, App
591	7	0.9	2303	5	US-10-852-335A-109	Sequence 109, App	664	7	0.9	3150	4	US-10-184-644-81	Sequence 81, Appl
592	7	0.9	2303	4	US-10-029-386-31982	Sequence 31982, A	665	7	0.9	3150	4	US-10-184-634-81	Sequence 81, Appl
593	7	0.9	2387	4	US-10-123-155-527	Sequence 527, App	666	7	0.9	3192	4	US-10-123-155-75	Sequence 75, Appl
594	7	0.9	2387	4	US-10-146-731-527	Sequence 527, App	667	7	0.9	3192	4	US-10-146-731-75	Sequence 75, Appl
595	7	0.9	2387	4	US-10-140-472-527	Sequence 527, App	668	7	0.9	3192	4	US-10-140-472-75	Sequence 75, Appl
596	7	0.9	2387	4	US-10-141-761-527	Sequence 527, App	669	7	0.9	3192	4	US-10-141-761-75	Sequence 75, Appl
597	7	0.9	2387	4	US-10-142-885-527	Sequence 527, App	670	7	0.9	3192	4	US-10-142-885-75	Sequence 75, Appl
598	7	0.9	2387	4	US-10-158-790-527	Sequence 527, App	671	7	0.9	3192	4	US-10-158-790-75	Sequence 75, Appl
599	7	0.9	2387	4	US-10-137-871-527	Sequence 527, App	672	7	0.9	3192	4	US-10-137-871-75	Sequence 75, Appl
600	7	0.9	2387	4	US-10-140-923-527	Sequence 527, App	673	7	0.9	3192	4	US-10-140-923-75	Sequence 75, Appl
601	7	0.9	2387	4	US-10-141-756-527	Sequence 527, App	674	7	0.9	3192	4	US-10-141-756-75	Sequence 75, Appl
602	7	0.9	2387	4	US-10-141-759-527	Sequence 527, App	675	7	0.9	3192	4	US-10-141-759-75	Sequence 75, Appl
603	7	0.9	2387	4	US-10-140-805-527	Sequence 527, App	676	7	0.9	3192	4	US-10-140-805-75	Sequence 75, Appl
604	7	0.9	2387	4	US-10-140-864-527	Sequence 527, App	677	7	0.9	3192	4	US-10-140-864-75	Sequence 75, Appl
605	7	0.9	2387	4	US-10-184-644-29	Sequence 29, Appl	678	7	0.9	3194	4	US-10-282-122A-59046	Sequence 59046, A
606	7	0.9	2397	4	US-10-184-634-323	Sequence 323, App	679	7	0.9	3194	4	US-10-123-155-81	Sequence 81, Appl
607	7	0.9	2397	4	US-10-184-634-323	Sequence 323, App	680	7	0.9	3233	4	US-10-146-731-81	Sequence 81, Appl
608	7	0.9	2397	4	US-10-184-634-323	Sequence 323, App	681	7	0.9	3233	4	US-10-140-472-81	Sequence 81, Appl
609	7	0.9	2397	4	US-10-063-685-107	Sequence 107, App	682	7	0.9	3233	4	US-10-141-761-81	Sequence 81, Appl
610	7	0.9	2397	4	US-10-063-685-107	Sequence 107, App	683	7	0.9	3233	4	US-10-142-885-81	Sequence 81, Appl
611	7	0.9	2431	3	US-09-901-106-2	Sequence 2, Appli	684	7	0.9	3233	4		

685	7	0.9	3233	4	US-10-158-790-81	Sequence 81, Appl	758	6	0.8	9	3	US-09-935-384-219	Sequence 219, App
686	7	0.9	3233	4	US-10-137-871-81	Sequence 81, Appl	759	6	0.8	9	3	US-09-935-384-447	Sequence 447, App
687	7	0.9	3233	4	US-10-140-923-81	Sequence 81, Appl	760	6	0.8	9	3	US-09-935-384-613	Sequence 613, App
688	7	0.9	3233	4	US-10-141-756-81	Sequence 81, Appl	761	6	0.8	10	3	US-09-572-404B-512	Sequence 512, App
689	7	0.9	3233	4	US-10-141-759-81	Sequence 81, Appl	762	6	0.8	10	3	US-09-935-384-158	Sequence 158, App
690	7	0.9	3233	4	US-10-140-805-81	Sequence 81, Appl	763	6	0.8	10	3	US-09-935-384-266	Sequence 266, App
691	7	0.9	3233	4	US-10-140-864-81	Sequence 81, Appl	764	6	0.8	10	3	US-09-935-384-268	Sequence 268, App
692	7	0.9	3240	4	US-10-184-644-415	Sequence 415, App	765	6	0.8	10	3	US-09-935-384-473	Sequence 473, App
693	7	0.9	3240	4	US-10-184-634-415	Sequence 415, App	766	6	0.8	10	3	US-09-935-384-573	Sequence 573, App
694	7	0.9	3323	4	US-10-123-155-167	Sequence 167, App	767	6	0.8	10	4	US-10-319-340-4	Sequence 4, Appli
695	7	0.9	3323	4	US-10-146-731-167	Sequence 167, App	768	6	0.8	10	4	US-10-319-340-5	Sequence 5, Appli
696	7	0.9	3323	4	US-10-140-472-167	Sequence 167, App	769	6	0.8	10	4	US-10-319-340-6	Sequence 6, Appli
697	7	0.9	3323	4	US-10-141-761-167	Sequence 167, App	770	6	0.8	10	4	US-10-319-340-19	Sequence 19, Appli
698	7	0.9	3323	4	US-10-142-885-167	Sequence 167, App	771	6	0.8	10	4	US-10-297-969-2	Sequence 2, Appli
699	7	0.9	3323	4	US-10-158-790-167	Sequence 167, App	772	6	0.8	11	5	US-10-862-195-2159	Sequence 2159, App
700	7	0.9	3323	4	US-10-137-871-167	Sequence 167, App	773	6	0.8	11	5	US-10-946-647-171	Sequence 171, App
701	7	0.9	3323	4	US-10-140-923-167	Sequence 167, App	774	6	0.8	11	5	US-10-946-647-399	Sequence 399, App
702	7	0.9	3323	4	US-10-141-756-167	Sequence 167, App	775	6	0.8	11	5	US-10-946-647-530	Sequence 530, App
703	7	0.9	3323	4	US-10-141-759-167	Sequence 167, App	776	6	0.8	11	5	US-10-946-647-700	Sequence 700, App
704	7	0.9	3323	4	US-10-140-805-167	Sequence 167, App	777	6	0.8	12	4	US-10-700-330-137	Sequence 137, App
705	7	0.9	3323	4	US-10-140-864-167	Sequence 167, App	778	6	0.8	13	4	US-10-411-869A-53	Sequence 53, Appl
706	7	0.9	3401	4	US-10-184-644-411	Sequence 411, App	779	6	0.8	14	4	US-10-312-691-6	Sequence 6, Appli
707	7	0.9	3401	4	US-10-184-634-411	Sequence 411, App	780	6	0.8	14	5	US-10-813-638-1304	Sequence 1304, Ap
708	7	0.9	3552	4	US-10-123-155-339	Sequence 339, App	781	6	0.8	15	3	US-09-880-748-2970	Sequence 2970, Ap
709	7	0.9	3552	4	US-10-146-731-339	Sequence 339, App	782	6	0.8	15	4	US-10-293-418-2970	Sequence 2970, Ap
710	7	0.9	3552	4	US-10-140-472-339	Sequence 339, App	783	6	0.8	15	4	US-10-412-964-68	Sequence 68, Appl
711	7	0.9	3552	4	US-10-141-761-339	Sequence 339, App	784	6	0.8	16	5	US-10-862-195-1036	Sequence 1036, Ap
712	7	0.9	3552	4	US-10-142-885-339	Sequence 339, App	785	6	0.8	18	4	US-10-187-496A-20	Sequence 20, Appl
713	7	0.9	3552	4	US-10-158-790-339	Sequence 339, App	786	6	0.8	18	5	US-10-946-647-402	Sequence 402, App
714	7	0.9	3552	4	US-10-137-871-339	Sequence 339, App	787	6	0.8	19	3	US-09-932-923-1	Sequence 1, Appli
715	7	0.9	3552	4	US-10-140-923-339	Sequence 339, App	788	6	0.8	19	4	US-10-297-969-6	Sequence 6, Appli
716	7	0.9	3552	4	US-10-141-756-339	Sequence 339, App	789	6	0.8	21	4	US-10-449-735-3	Sequence 3, Appli
717	7	0.9	3552	4	US-10-141-759-339	Sequence 339, App	790	6	0.8	23	4	US-10-097-065-356	Sequence 356, App
718	7	0.9	3552	4	US-10-140-805-339	Sequence 339, App	791	6	0.8	23	4	US-10-372-876-356	Sequence 356, App
719	7	0.9	3552	4	US-10-140-864-339	Sequence 339, App	792	6	0.8	24	3	US-09-843-221A-129	Sequence 129, App
720	7	0.9	3871	4	US-10-184-644-347	Sequence 347, App	793	6	0.8	24	3	US-09-843-221A-130	Sequence 130, App
721	7	0.9	3871	4	US-10-184-634-347	Sequence 347, App	794	6	0.8	24	3	US-09-999-608-129	Sequence 129, App
722	7	0.9	4040	4	US-10-123-155-425	Sequence 425, App	795	6	0.8	24	3	US-09-999-608-130	Sequence 130, App
723	7	0.9	4040	4	US-10-146-731-425	Sequence 425, App	796	6	0.8	24	4	US-10-425-115-338692	Sequence 338692,
724	7	0.9	4040	4	US-10-140-472-425	Sequence 425, App	797	6	0.8	24	4	US-10-839-037-129	Sequence 129, App
725	7	0.9	4040	4	US-10-141-761-425	Sequence 425, App	798	6	0.8	24	4	US-10-839-037-130	Sequence 130, App
726	7	0.9	4040	4	US-10-142-885-425	Sequence 425, App	799	6	0.8	25	3	US-09-911-888-35	Sequence 35, Appl
727	7	0.9	4040	4	US-10-158-790-425	Sequence 425, App	800	6	0.8	25	3	US-09-911-927-35	Sequence 35, Appl
728	7	0.9	4040	4	US-10-137-871-425	Sequence 425, App	801	6	0.8	26	4	US-10-242-355-472	Sequence 472, App
729	7	0.9	4040	4	US-10-140-923-425	Sequence 425, App	802	6	0.8	26	5	US-10-946-647-1362	Sequence 1362, Ap
730	7	0.9	4040	4	US-10-141-756-425	Sequence 425, App	803	6	0.8	28	3	US-09-843-221A-93	Sequence 93, Appl
731	7	0.9	4040	4	US-10-141-759-425	Sequence 425, App	804	6	0.8	28	3	US-09-843-221A-94	Sequence 94, Appl
732	7	0.9	4040	4	US-10-140-805-425	Sequence 425, App	805	6	0.8	28	3	US-09-999-608-93	Sequence 93, Appl
733	7	0.9	4040	4	US-10-140-864-425	Sequence 425, App	806	6	0.8	28	3	US-09-999-608-94	Sequence 94, Appl
734	7	0.9	4060	4	US-10-123-155-197	Sequence 197, App	807	6	0.8	28	4	US-10-261-208-4	Sequence 4, Appli
735	7	0.9	4060	4	US-10-146-731-197	Sequence 197, App	808	6	0.8	28	4	US-10-424-599-156146	Sequence 156146,
736	7	0.9	4060	4	US-10-140-472-197	Sequence 197, App	809	6	0.8	28	4	US-10-839-037-93	Sequence 93, Appl
737	7	0.9	4060	4	US-10-141-761-197	Sequence 197, App	810	6	0.8	28	4	US-10-839-037-94	Sequence 94, Appl
738	7	0.9	4060	4	US-10-142-885-197	Sequence 197, App	811	6	0.8	28	5	US-10-926-683-1203	Sequence 1203, Ap
739	7	0.9	4060	4	US-10-158-790-197	Sequence 197, App	812	6	0.8	28	5	US-10-915-740A-1051	Sequence 1051, Ap
740	7	0.9	4060	4	US-10-137-871-197	Sequence 197, App	813	6	0.8	30	3	US-09-843-221A-124	Sequence 124, App
741	7	0.9	4060	4	US-10-140-923-197	Sequence 197, App	814	6	0.8	30	3	US-09-843-221A-125	Sequence 125, App
742	7	0.9	4060	4	US-10-141-756-197	Sequence 197, App	815	6	0.8	30	3	US-09-843-221A-158	Sequence 158, App
743	7	0.9	4060	4	US-10-141-759-197	Sequence 197, App	816	6	0.8	30	3	US-09-999-608-124	Sequence 124, App
744	7	0.9	4060	4	US-10-140-805-197	Sequence 197, App	817	6	0.8	30	3	US-09-999-608-125	Sequence 125, App
745	7	0.9	4060	4	US-10-140-864-197	Sequence 197, App	818	6	0.8	30	3	US-09-999-608-158	Sequence 158, App
746	7	0.9	4106	3	US-09-980-217-23	Sequence 23, Appl	819	6	0.8	30	4	US-10-437-963-138633	Sequence 138633,
747	7	0.9	4106	5	US-10-732-923-20549	Sequence 20549, A	820	6	0.8	30	4	US-10-839-037-124	Sequence 124, App
748	7	0.9	4640	4	US-10-184-644-75	Sequence 75, Appl	821	6	0.8	30	4	US-10-839-037-125	Sequence 125, App
749	7	0.9	4640	4	US-10-184-634-75	Sequence 75, Appl	822	6	0.8	31	4	US-10-839-037-158	Sequence 158, App
750	7	0.9	4679	3	US-09-804-898-2	Sequence 2, Appli	823	6	0.8	31	4	US-10-097-079-50	Sequence 50, Appl
751	7	0.9	4999	3	US-09-976-059-14	Sequence 14, Appl	824	6	0.8	33	3	US-09-864-761-35842	Sequence 35842, A
752	7	0.9	8026	4	US-10-132-134-12	Sequence 12, Appl	825	6	0.8	33	4	US-10-000-256A-175	Sequence 175, App
753	7	0.9	18636	4	US-10-073-912-17	Sequence 17, Appl	826	6	0.8	33	4	US-10-029-386-33592	Sequence 33592, A
754	7	0.9	35346	5	US-10-874-049-2	Sequence 2, Appli	827	6	0.8	33	4	US-10-424-599-205494	Sequence 205494,
755	7	0.9	35823	5	US-10-874-049-1	Sequence 1, Appli	828	6	0.8	34	3	US-09-843-221A-88	Sequence 88, Appl
756	7	0.9	36946	5	US-10-840-512-155	Sequence 155, App	829	6	0.8	34	3	US-09-843-221A-89	Sequence 89, Appl
757	6	0.8	9	3	US-09-935-384-116	Sequence 116, App	830	6	0.8	34	3	US-09-843-221A-122	Sequence 122, App

831	6	0.8	34	3	US-09-935-384-755	Sequence 755, App	904	6	0.8	53	4	US-10-425-115-273363	Sequence 273363,
832	6	0.8	34	3	US-09-935-384-756	Sequence 756, App	905	6	0.8	54	4	US-10-424-599-192315	Sequence 192315,
833	6	0.8	34	3	US-09-999-608-88	Sequence 88, App1	906	6	0.8	54	4	US-10-424-599-236359	Sequence 236359,
834	6	0.8	34	3	US-09-999-608-89	Sequence 89, App1	907	6	0.8	54	4	US-10-425-115-211925	Sequence 211925,
835	6	0.8	34	3	US-09-999-608-122	Sequence 122, App	908	6	0.8	54	4	US-10-425-115-261837	Sequence 261837,
836	6	0.8	34	4	US-10-282-122A-70169	Sequence 70169, A	909	6	0.8	54	4	US-10-425-115-308996	Sequence 308996,
837	6	0.8	34	4	US-10-425-115-265306	Sequence 265306,	910	6	0.8	54	4	US-10-425-115-33948	Sequence 33948,
838	6	0.8	34	4	US-10-839-037-88	Sequence 88, App1	911	6	0.8	54	5	US-10-808-187-1904	Sequence 1904, App
839	6	0.8	34	4	US-10-839-037-89	Sequence 89, App1	912	6	0.8	54	5	US-10-807-807-1904	Sequence 1904, App
840	6	0.8	34	4	US-10-839-037-122	Sequence 122, App	913	6	0.8	55	3	US-09-864-761-47472	Sequence 47472, A
841	6	0.8	34	4	US-10-425-115-356970	Sequence 356970,	914	6	0.8	55	4	US-10-424-599-150228	Sequence 150228,
842	6	0.8	36	3	US-09-864-761-35450	Sequence 35450, A	915	6	0.8	55	4	US-10-425-115-281675	Sequence 281675,
843	6	0.8	36	4	US-10-437-963-134795	Sequence 134795,	916	6	0.8	56	3	US-09-864-761-38992	Sequence 38992, A
844	6	0.8	36	4	US-10-437-963-195293	Sequence 195293,	917	6	0.8	56	3	US-09-939-980-332	Sequence 332, App
845	6	0.8	36	4	US-10-425-115-227274	Sequence 227274,	918	6	0.8	56	4	US-10-424-599-181170	Sequence 181170,
846	6	0.8	36	4	US-10-425-115-263124	Sequence 263124,	919	6	0.8	56	4	US-10-424-599-196379	Sequence 196379,
847	6	0.8	38	3	US-09-864-761-33780	Sequence 33780, A	920	6	0.8	56	4	US-10-424-599-211496	Sequence 211496,
848	6	0.8	39	4	US-10-029-386-30437	Sequence 30437, A	921	6	0.8	56	4	US-10-424-599-193169	Sequence 193169,
849	6	0.8	39	4	US-10-425-115-367446	Sequence 367446,	922	6	0.8	57	3	US-09-864-761-46468	Sequence 46468, A
850	6	0.8	40	4	US-10-424-599-158157	Sequence 158157,	923	6	0.8	57	4	US-10-424-599-155487	Sequence 155487,
851	6	0.8	40	4	US-10-724-972A-5238	Sequence 5238, App	924	6	0.8	57	4	US-10-424-599-249260	Sequence 249260,
852	6	0.8	41	4	US-10-424-599-159947	Sequence 159947,	925	6	0.8	57	4	US-10-437-963-104783	Sequence 104783,
853	6	0.8	41	4	US-10-424-599-170123	Sequence 170123,	926	6	0.8	57	4	US-10-437-963-145277	Sequence 145277,
854	6	0.8	42	4	US-10-424-599-238198	Sequence 238198,	927	6	0.8	57	4	US-10-425-115-335915	Sequence 335915,
855	6	0.8	42	4	US-10-424-599-269505	Sequence 269505,	928	6	0.8	58	4	US-10-425-115-218982	Sequence 218982,
856	6	0.8	42	4	US-10-424-599-270459	Sequence 270459,	929	6	0.8	58	4	US-10-425-115-218982	Sequence 316296,
857	6	0.8	42	4	US-10-425-115-273437	Sequence 273437,	930	6	0.8	58	4	US-10-425-115-316296	Sequence 316296,
858	6	0.8	43	4	US-10-424-599-254844	Sequence 254844,	931	6	0.8	58	5	US-10-450-763-52557	Sequence 52557, A
859	6	0.8	43	4	US-10-767-701-61514	Sequence 61514, A	932	6	0.8	59	3	US-09-864-761-42686	Sequence 42686, A
860	6	0.8	43	4	US-10-425-115-284961	Sequence 284961,	933	6	0.8	59	4	US-10-424-599-187445	Sequence 187445,
861	6	0.8	44	3	US-09-925-299-1094	Sequence 1094, App	934	6	0.8	59	4	US-10-437-963-196161	Sequence 196161,
862	6	0.8	44	3	US-09-925-299-1094	Sequence 1094, App	935	6	0.8	59	4	US-10-767-701-33262	Sequence 33262, A
863	6	0.8	44	3	US-10-083-357-858	Sequence 858, App	936	6	0.8	59	4	US-10-425-115-230151	Sequence 230151,
864	6	0.8	44	4	US-10-097-111-462	Sequence 462, App	937	6	0.8	59	4	US-10-425-115-268417	Sequence 268417,
865	6	0.8	44	4	US-10-424-599-181073	Sequence 181073,	938	6	0.8	59	4	US-10-425-115-326057	Sequence 326057,
866	6	0.8	44	4	US-10-424-599-208117	Sequence 208117,	939	6	0.8	59	6	US-11-087-143-34938	Sequence 34938, A
867	6	0.8	44	4	US-10-424-599-228849	Sequence 228849,	940	6	0.8	60	3	US-09-864-761-36505	Sequence 36505, A
868	6	0.8	45	4	US-10-424-599-200405	Sequence 200405,	941	6	0.8	60	3	US-09-935-384-773	Sequence 773, App
869	6	0.8	45	4	US-10-424-599-192929	Sequence 192929,	942	6	0.8	60	3	US-09-935-384-774	Sequence 774, App
870	6	0.8	46	4	US-10-424-599-152929	Sequence 152929,	943	6	0.8	60	3	US-10-166-698-5226	Sequence 5226, App
871	6	0.8	46	4	US-10-424-599-250018	Sequence 250018,	944	6	0.8	60	4	US-10-166-698-5226	Sequence 217289,
872	6	0.8	46	4	US-10-424-599-284367	Sequence 284367,	945	6	0.8	60	4	US-10-424-599-217289	Sequence 265017,
873	6	0.8	47	4	US-10-424-599-164462	Sequence 164462,	946	6	0.8	60	4	US-10-424-599-265017	Sequence 275730,
874	6	0.8	47	4	US-10-424-599-175289	Sequence 175289,	947	6	0.8	60	4	US-10-424-599-275730	Sequence 278739,
875	6	0.8	47	4	US-10-424-599-214676	Sequence 214676,	948	6	0.8	60	4	US-10-424-599-278739	Sequence 33, App1
876	6	0.8	49	4	US-10-424-599-247006	Sequence 247006,	949	6	0.8	60	4	US-10-466-205-33	Sequence 15, App1
877	6	0.8	49	4	US-10-425-115-201029	Sequence 201029,	950	6	0.8	60	4	US-10-240-801A-15	Sequence 15, App1
878	6	0.8	49	4	US-10-425-115-212882	Sequence 212882,	951	6	0.8	60	4	US-10-437-963-145637	Sequence 145637,
879	6	0.8	49	4	US-10-425-115-343792	Sequence 343792,	952	6	0.8	60	4	US-10-490-917-1	Sequence 1, App1
880	6	0.8	50	4	US-10-424-599-142892	Sequence 142892,	953	6	0.8	60	4	US-10-425-115-249337	Sequence 249337,
881	6	0.8	50	4	US-10-437-963-143258	Sequence 143258,	954	6	0.8	60	4	US-10-425-115-258455	Sequence 258455,
882	6	0.8	50	4	US-10-437-963-144934	Sequence 144934,	955	6	0.8	60	4	US-10-425-115-282677	Sequence 282677,
883	6	0.8	50	4	US-10-425-115-246059	Sequence 246059,	956	6	0.8	60	4	US-10-425-115-282677	Sequence 282677,
884	6	0.8	50	4	US-10-425-115-258548	Sequence 258548,	957	6	0.8	60	4	US-10-425-115-340928	Sequence 340928,
885	6	0.8	50	4	US-10-425-115-289140	Sequence 289140,	958	6	0.8	61	4	US-10-424-599-216350	Sequence 216350,
886	6	0.8	50	4	US-10-425-115-345542	Sequence 345542,	959	6	0.8	61	4	US-10-425-115-225088	Sequence 225088,
887	6	0.8	51	3	US-09-864-761-41434	Sequence 41434, A	960	6	0.8	61	4	US-10-425-115-273735	Sequence 273735,
888	6	0.8	51	3	US-09-864-761-41434	Sequence 41434, A	961	6	0.8	61	4	US-10-425-115-351161	Sequence 351161,
889	6	0.8	51	3	US-09-738-626-4205	Sequence 4205, App	962	6	0.8	62	4	US-10-424-599-178215	Sequence 178215,
890	6	0.8	51	4	US-10-424-599-188733	Sequence 188733,	963	6	0.8	62	4	US-10-424-599-244018	Sequence 244018,
891	6	0.8	51	4	US-10-424-599-192988	Sequence 192988,	964	6	0.8	62	4	US-10-424-599-246325	Sequence 246325,
892	6	0.8	51	4	US-10-425-115-229574	Sequence 229574,	965	6	0.8	62	4	US-10-425-115-226730	Sequence 226730,
893	6	0.8	51	4	US-10-425-115-281091	Sequence 281091,	966	6	0.8	62	4	US-10-425-115-251725	Sequence 251725,
894	6	0.8	52	3	US-09-764-847-804	Sequence 804, App	967	6	0.8	62	4	US-10-425-115-280551	Sequence 280551,
895	6	0.8	52	4	US-10-092-154-804	Sequence 804, App	968	6	0.8	63	3	US-09-864-761-48451	Sequence 48451, A
896	6	0.8	52	4	US-10-029-386-32686	Sequence 32686, A	969	6	0.8	63	3	US-09-738-626-5130	Sequence 5130, App
897	6	0.8	52	4	US-10-424-599-210870	Sequence 210870,	970	6	0.8	63	3	US-09-738-626-5130	Sequence 354, App
898	6	0.8	52	4	US-10-424-599-241749	Sequence 241749,	971	6	0.8	63	4	US-10-074-095-354	Sequence 354, App
899	6	0.8	52	4	US-10-437-963-135363	Sequence 135363,	972	6	0.8	63	4	US-10-212-872-354	Sequence 354, App
900	6	0.8	52	4	US-10-437-963-183149	Sequence 183149,	973	6	0.8	63	4	US-10-424-599-198003	Sequence 198003,
901	6	0.8	52	4	US-10-767-701-59635	Sequence 59635, A	974	6	0.8	63	4	US-10-424-599-232260	Sequence 232260,
902	6	0.8	53	4	US-10-424-599-233874	Sequence 233874,	975	6	0.8	63	4	US-10-424-599-239634	Sequence 239634,
903	6	0.8	53	4	US-10-425-115-209875	Sequence 209875,	976	6	0.8	63	4	US-10-425-115-185582	Sequence 185582,

977	6	0.8	63	4	US-10-425-115-207449	Sequence 207449,
978	6	0.8	63	4	US-10-425-115-265999	Sequence 265999,
979	6	0.8	63	4	US-10-425-115-293345	Sequence 293345,
980	6	0.8	64	4	US-10-349-607-130	Sequence 130, App
981	6	0.8	64	4	US-10-424-599-154815	Sequence 154815,
982	6	0.8	64	4	US-10-425-115-234850	Sequence 234850,
983	6	0.8	64	4	US-10-425-115-255147	Sequence 255147,
984	6	0.8	64	4	US-10-425-115-312105	Sequence 312105,
985	6	0.8	65	3	US-09-864-761-39981	Sequence 39981, A
986	6	0.8	65	4	US-10-001-870-119	Sequence 119, App
987	6	0.8	65	4	US-10-097-111-388	Sequence 388, App
988	6	0.8	65	4	US-10-425-115-279901	Sequence 279901,
989	6	0.8	65	5	US-10-856-499-604	Sequence 604, App
990	6	0.8	66	4	US-10-424-599-193996	Sequence 193996,
991	6	0.8	66	4	US-10-424-599-198991	Sequence 198991,
992	6	0.8	66	4	US-10-424-599-223134	Sequence 223134,
993	6	0.8	66	4	US-10-425-115-336417	Sequence 336417,
994	6	0.8	67	4	US-10-156-761-8250	Sequence 8250, Ap
995	6	0.8	67	4	US-10-424-599-160950	Sequence 160950,
996	6	0.8	67	4	US-10-424-599-261870	Sequence 261870,
997	6	0.8	67	4	US-10-424-599-266764	Sequence 266764,
998	6	0.8	67	4	US-10-425-115-313696	Sequence 313696,
999	6	0.8	67	5	US-10-450-763-55517	Sequence 55517, A
1000	6	0.8	68	4	US-10-424-599-205787	Sequence 205787,

ALIGNMENTS

977	6	0.8	63	4	US-09-994-192-4	Sequence 4, Application US/09994192
978	6	0.8	63	4	US-09-994-192-4	Publication No. US20020086028A1
979	6	0.8	63	4	US-09-994-192-4	GENERAL INFORMATION:
980	6	0.8	63	4	US-09-994-192-4	APPLICANT: Judd, Ralph C.
981	6	0.8	63	4	US-09-994-192-4	APPLICANT: Manning, Scott D.
982	6	0.8	63	4	US-09-994-192-4	TITLE OF INVENTION: Omp85 Proteins of Neisseria gonorrhoeae and Neisseria meningitidis
983	6	0.8	63	4	US-09-994-192-4	TITLE OF INVENTION: Compositions Containing Same and Methods of Use Thereof
984	6	0.8	63	4	US-09-994-192-4	FILE REFERENCE: USBC147AUSA
985	6	0.8	63	4	US-09-994-192-4	CURRENT APPLICATION NUMBER: US/09/994,192
986	6	0.8	63	4	US-09-994-192-4	PRIOR FILING DATE: 2001-11-26
987	6	0.8	63	4	US-09-994-192-4	PRIOR FILING DATE: 2001-11-26
988	6	0.8	63	4	US-09-994-192-4	PRIOR FILING DATE: 1998-10-22
989	6	0.8	63	4	US-09-994-192-4	NUMBER OF SEQ ID NOS: 8
990	6	0.8	63	4	US-09-994-192-4	SOFTWARE: Patent in version 3.1
991	6	0.8	63	4	US-09-994-192-4	SEQ ID NO 4
992	6	0.8	63	4	US-09-994-192-4	LENGTH: 797
993	6	0.8	63	4	US-09-994-192-4	TYPE: PRT
994	6	0.8	63	4	US-09-994-192-4	ORGANISM: Neisseria meningitidis
995	6	0.8	63	4	US-09-994-192-4	US-09-994-192-4

Query Match 100.0%; Score 797; DB 3; Length 797;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPEPSTVFNYLPVKVGDYNDTHGSA	60
Db	1	MLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPEPSTVFNYLPVKVGDYNDTHGSA	60
Qy	61	IIKSLYATGFFDDVRVETADGQLLTVTIERPTIGSLNITGAKMLONDAIKKNLESFCLAQ	120
Db	61	IIKSLYATGFFDDVRVETADGQLLTVTIERPTIGSLNITGAKMLONDAIKKNLESFCLAQ	120
Qy	121	SOYFNQATLNQAVAGLKEEYLGRLKNIQITPKVTKLARNRVDITIDEGSKAKITDIE	180
Db	121	SOYFNQATLNQAVAGLKEEYLGRLKNIQITPKVTKLARNRVDITIDEGSKAKITDIE	180
Qy	181	PEGNQVTSRDLKMRQMSLTGEGITWLTNRNQFQKPAQDMKQVTFYQNNGYFDFRIL	240
Db	181	PEGNQVTSRDLKMRQMSLTGEGITWLTNRNQFQKPAQDMKQVTFYQNNGYFDFRIL	240
Qy	241	DTDIQTNEDKTKQTIKTVHEGGRFRWGKVSIEGDTNEVPKAELEKLLTMKPGKMYERQ	300
Db	241	DTDIQTNEDKTKQTIKTVHEGGRFRWGKVSIEGDTNEVPKAELEKLLTMKPGKMYERQ	300

241	Db	241	DTDIQTNEDKTKQTIKTVHEGGRFRWGKVSIEGDTNEVPKAELEKLLTMKPGKMYERQ	300
301	Qy	301	MTAVLGEIQNRMGSGAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEHIITGNKT	360
301	Db	301	MTAVLGEIQNRMGSGAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEHIITGNKT	360
361	Qy	361	RDVVRELRQWESABYDTSKLQSKERVVELLGYFDNVQFDVAPLAGTDPKVDLNNSLTE	420
361	Db	361	RDVVRELRQWESABYDTSKLQSKERVVELLGYFDNVQFDVAPLAGTDPKVDLNNSLTE	420
421	Qy	421	RSTGSLDLGAGWQDTGLVMSAGVSQDNLFGTGKSAALRASRSKTTLNGSLSFDPYFTA	480
421	Db	421	RSTGSLDLGAGWQDTGLVMSAGVSQDNLFGTGKSAALRASRSKTTLNGSLSFDPYFTA	480
481	Qy	481	DGVSIGDYVYGKAFDPKPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT	540
481	Db	481	DGVSIGDYVYGKAFDPKPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT	540
541	Qy	541	YNKAPKHYADFIKYGKTDGTSFGKWLKGTGVGGRNKTDLSALWPTRGYLTGVNAEIA	600
541	Db	541	YNKAPKHYADFIKYGKTDGTSFGKWLKGTGVGGRNKTDLSALWPTRGYLTGVNAEIA	600
601	Qy	601	LPGSKLQYYSATHNQTFWFFPLSKTFTMLGGEVGIAGGYGRTKEIPFFENFYGGGLGSVR	660
601	Db	601	LPGSKLQYYSATHNQTFWFFPLSKTFTMLGGEVGIAGGYGRTKEIPFFENFYGGGLGSVR	660
661	Qy	661	GYESGTLGPKVDEYGEKISYCGNKKANYSAELLFPMPCAKDARTVRLSLFADAGSVWDG	720
661	Db	661	GYESGTLGPKVDEYGEKISYCGNKKANYSAELLFPMPCAKDARTVRLSLFADAGSVWDG	720
721	Qy	721	KTYDDNSSATGGRVQNIYAGNTHKSTFTNELRYSAGGAVTWLSPLGPMKPRYAYPLKK	780
721	Db	721	KTYDDNSSATGGRVQNIYAGNTHKSTFTNELRYSAGGAVTWLSPLGPMKPRYAYPLKK	780
781	Qy	781	KPEDEIQRFQFQLGTTTF 797	
781	Db	781	KPEDEIQRFQFQLGTTTF 797	

RESULT 2

US-10-606-618-4

Sequence 4, Application US/10606618

Publication No. US20050074458A1

GENERAL INFORMATION:

APPLICANT: Judd, Ralph C.

APPLICANT: Manning, Scott D.

TITLE OF INVENTION: Omp85 Proteins of Neisseria gonorrhoeae and Neisseria meningitidis

TITLE OF INVENTION: Compositions Containing Same and Methods of Use Thereof

FILE REFERENCE: USBC147AUSA

CURRENT APPLICATION NUMBER: US/10/606,618

CURRENT FILING DATE: 2003-06-26

PRIOR APPLICATION NUMBER: US/09/994,192

PRIOR FILING DATE: 2001-11-26

PRIOR APPLICATION NUMBER: US 09/177,039

PRIOR FILING DATE: 1998-10-22

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patent in version 3.1

SEQ ID NO 4

LENGTH: 797

TYPE: PRT

ORGANISM: Neisseria meningitidis

US-10-606-618-4

Query Match 100.0%; Score 797; DB 5; Length 797;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPEPSTVFNYLPVKVGDYNDTHGSA	60
Db	1	MLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPEPSTVFNYLPVKVGDYNDTHGSA	60
Qy	61	IIKSLYATGFFDDVRVETADGQLLTVTIERPTIGSLNITGAKMLONDAIKKNLESFCLAQ	120
Db	61	IIKSLYATGFFDDVRVETADGQLLTVTIERPTIGSLNITGAKMLONDAIKKNLESFCLAQ	120
Qy	121	SOYFNQATLNQAVAGLKEEYLGRLKNIQITPKVTKLARNRVDITIDEGSKAKITDIE	180
Db	121	SOYFNQATLNQAVAGLKEEYLGRLKNIQITPKVTKLARNRVDITIDEGSKAKITDIE	180
Qy	181	PEGNQVTSRDLKMRQMSLTGEGITWLTNRNQFQKPAQDMKQVTFYQNNGYFDFRIL	240
Db	181	PEGNQVTSRDLKMRQMSLTGEGITWLTNRNQFQKPAQDMKQVTFYQNNGYFDFRIL	240
Qy	241	DTDIQTNEDKTKQTIKTVHEGGRFRWGKVSIEGDTNEVPKAELEKLLTMKPGKMYERQ	300
Db	241	DTDIQTNEDKTKQTIKTVHEGGRFRWGKVSIEGDTNEVPKAELEKLLTMKPGKMYERQ	300



Db 61 I I K S L Y A T G P D D V R V E T A D Q L L L T V I E R P T I G S L N I T G A K M L Q N D A I K K N L S F G L A Q 120  
Qy 121 S O Y F N Q A T L N Q A V A G L K E E Y L G R G K L N I Q I T P K V T K L A R N R V D I D I I D E G K S A K I T D I E 180  
Db 121 S O Y F N Q A T L N Q A V A G L K E E Y L G R G K L N I Q I T P K V T K L A R N R V D I D I I D E G K S A K I T D I E 180  
Qy 181 F E G N Q V S D R K L M Q M S I T E G I I T W L T R S N Q F N E Q K F A Q D M E K V T D F Y Q N N G Y F D F R I L 240  
Db 181 F E G N Q V S D R K L M Q M S I T E G I I T W L T R S N Q F N E Q K F A Q D M E K V T D F Y Q N N G Y F D F R I L 240  
Qy 241 D T D I Q T N E D K T Q I K I T V H E G G R F M G K V S I E G D T N E V P K A E L K L L T M K P G K W Y R Q Q 300  
Db 241 D T D I Q T N E D K T Q I K I T V H E G G R F M G K V S I E G D T N E V P K A E L K L L T M K P G K W Y R Q Q 300  
Qy 301 M T A V L G E I Q N R M S G A Y A S E I S V Q P L P N A E T K T V D F V L H I E P G R K I Y V N E I H I T G N N K T 360  
Db 301 M T A V L G E I Q N R M S G A Y A S E I S V Q P L P N A E T K T V D F V L H I E P G R K I Y V N E I H I T G N N K T 360  
Qy 361 R D E V V R R E L R O M E S A P Y D T S K L Q R S K E R V E L L G Y F D N V Q F D A V P L A G T P D K V D L N M S L T E 420  
Db 361 R D E V V R R E L R O M E S A P Y D T S K L Q R S K E R V E L L G Y F D N V Q F D A V P L A G T P D K V D L N M S L T E 420  
Qy 421 R S T G S L D L S A G W Q D T G L V M S A G V S Q D N L F G T G K S A A L R A S R S K T T L N G S L S F T D P Y F T A 480  
Db 421 R S T G S L D L S A G W Q D T G L V M S A G V S Q D N L F G T G K S A A L R A S R S K T T L N G S L S F T D P Y F T A 480  
Qy 481 D G V S L G Y D V Y G K A F D P R K A S T S I K Q Y K T T T A G A G I R M S V P T E Y D R V N F G L V A E H L T V N T 540  
Db 481 D G V S L G Y D V Y G K A F D P R K A S T S I K Q Y K T T T A G A G I R M S V P T E Y D R V N F G L V A E H L T V N T 540  
Qy 541 Y N K A P K H Y A D F I K K Y G K T D G T D G S P K G W L Y K G T V G W G R N K T D S A L W P T R G Y L T G V N A E I A 600  
Db 541 Y N K A P K H Y A D F I K K Y G K T D G T D G S P K G W L Y K G T V G W G R N K T D S A L W P T R G Y L T G V N A E I A 600  
Qy 601 L P G S K L O Y S A T H N Q T W F P L S K T F T L M L G G E V G I A G G Y G R T K E I P F F E N F Y G G L G S V R 660  
Db 601 L P G S K L O Y S A T H N Q T W F P L S K T F T L M L G G E V G I A G G Y G R T K E I P F F E N F Y G G L G S V R 660  
Qy 661 G Y E S G T L G P K V Y D E Y G E K I S Y G G N K K A N V S A E L L F P M P G A K D A R T V R L S L F A D A G S V M D G 720  
Db 661 G Y E S G T L G P K V Y D E Y G E K I S Y G G N K K A N V S A E L L F P M P G A K D A R T V R L S L F A D A G S V M D G 720  
Qy 721 K T Y D N S S A T G G R V Q N I Y G A G N T H K S T F T N E L R Y S A G A V T W L S P L G P M K F R Y A Y P L K K 780  
Db 721 K T Y D N S S A T G G R V Q N I Y G A G N T H K S T F T N E L R Y S A G A V T W L S P L G P M K F R Y A Y P L K K 780  
Qy 781 K P E D E I Q R F O F O L G T T F 797  
Db 781 K P E D E I Q R F O F O L G T T F 797

RESULT 3  
US-10-181-660-3  
; Sequence 3, Application US/10181660  
; Publication No. US20030027097A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON Spa  
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS  
; FILE REFERENCE: P023785W0  
; CURRENT APPLICATION NUMBER: US/10/181,660  
; CURRENT FILING DATE: 2003-03-31  
; PRIOR APPLICATION NUMBER: GB-0001067.8  
; PRIOR FILING DATE: 2000-01-17  
; PRIOR APPLICATION NUMBER: GB-0005699.4  
; PRIOR FILING DATE: 2000-03-09  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: SeqWin99, version 1.02  
; SEQ ID NO 3  
; LENGTH: 797  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-10-181-660-3

Query Match 94.4%; Score 752; DB 4; Length 797;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 21 A D F T I Q D I R V E G L O R T E P S T V F N Y L P V K Y G D T Y N D T H G S A I I K S L Y A T G F D D V R V E T A D 80  
Db 21 A D F T I Q D I R V E G L O R T E P S T V F N Y L P V K Y G D T Y N D T H G S A I I K S L Y A T G F D D V R V E T A D 80  
Qy 81 G O L L L T V I E R P T I G S L N I T G A K M L Q N D A I K K N L S F G L A Q S O Y F N Q A T L N Q A V A G L K E E Y 140  
Db 81 G O L L L T V I E R P T I G S L N I T G A K M L Q N D A I K K N L S F G L A Q S O Y F N Q A T L N Q A V A G L K E E Y 140  
Qy 141 L G R G K L N I Q I T P K V T K L A R N R V D I D I I D E G K S A K I T D I E F E G N Q V S D R K L M Q M S L T E 200  
Db 141 L G R G K L N I Q I T P K V T K L A R N R V D I D I I D E G K S A K I T D I E F E G N Q V S D R K L M Q M S L T E 200  
Qy 201 G G I T W L T R S N Q F N E Q K F A Q D M E K V T D F Y Q N N G Y F D F R I L D T I Q T N E D K T Q I K I T V H 260  
Db 201 G G I T W L T R S N Q F N E Q K F A Q D M E K V T D F Y Q N N G Y F D F R I L D T I Q T N E D K T Q I K I T V H 260  
Qy 261 E G G R F M G K V S I E G D T N E V P K A E L K L L T M K P G K W Y R Q Q T A V L G E I Q N R M S G A Y A S 320  
Db 261 E G G R F M G K V S I E G D T N E V P K A E L K L L T M K P G K W Y R Q Q T A V L G E I Q N R M S G A Y A S 320  
Qy 321 E I S V Q P L P N A E T K T V D F V L H I E P G R K I Y V N E I H I T G N N K T R D E V V R R E L R O M E S A P Y D T S 380  
Db 321 E I S V Q P L P N A E T K T V D F V L H I E P G R K I Y V N E I H I T G N N K T R D E V V R R E L R O M E S A P Y D T S 380  
Qy 381 K L Q R S K E R V E L L G Y F D N V Q F D A V P L A G T P D K V D L N M S L T E R S T G S L D L S A G W Q D T G L V M 440  
Db 381 K L Q R S K E R V E L L G Y F D N V Q F D A V P L A G T P D K V D L N M S L T E R S T G S L D L S A G W Q D T G L V M 440  
Qy 441 S A G V S Q D N L F G T G K S A A L R A S R S K T T L N G S L S F T D P Y F T A D G V S L G Y D V Y G K A F D P R K A S 500  
Db 441 S A G V S Q D N L F G T G K S A A L R A S R S K T T L N G S L S F T D P Y F T A D G V S L G Y D V Y G K A F D P R K A S 500  
Qy 501 T S I K Q Y K T T T A G A G I R M S V P T E Y D R V N F G L V A E H L T V N T Y N K A P K H Y A D F I K K Y G K T D G 560  
Db 501 T S I K Q Y K T T T A G A G I R M S V P T E Y D R V N F G L V A E H L T V N T Y N K A P K H Y A D F I K K Y G K T D G 560  
Qy 561 T D G S F K G W L Y K G T V G W G R N K T D S A L W P T R G Y L T G V N A E I A L P G S K L O Y S A T H N Q T W F P P 620  
Db 561 T D G S F K G W L Y K G T V G W G R N K T D S A L W P T R G Y L T G V N A E I A L P G S K L O Y S A T H N Q T W F P P 620  
Qy 621 L S K T F T L M L G G E V G I A G G Y G R T K E I P F F E N F Y G G L G S V R G Y E S G T L G P K V Y D E Y G E K I S 680  
Db 621 L S K T F T L M L G G E V G I A G G Y G R T K E I P F F E N F Y G G L G S V R G Y E S G T L G P K V Y D E Y G E K I S 680  
Qy 681 Y G G N K K A N V S A E L L F P M P G A K D A R T V R L S L F A D A G S V M D G K T Y D N S S A T G G R V Q N I Y G 740  
Db 681 Y G G N K K A N V S A E L L F P M P G A K D A R T V R L S L F A D A G S V M D G K T Y D N S S A T G G R V Q N I Y G 740  
Qy 741 A G N T H K S T F T N E L R Y S A G A V T W L S P L G P M K F 772  
Db 741 A G N T H K S T F T N E L R Y S A G A V T W L S P L G P M K F 772

RESULT 4  
US-10-181-660-11  
; Sequence 11, Application US/10181660  
; Publication No. US20030027097A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON Spa  
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS  
; FILE REFERENCE: P023785W0  
; CURRENT APPLICATION NUMBER: US/10/181,660  
; CURRENT FILING DATE: 2003-03-31  
; PRIOR APPLICATION NUMBER: GB-0001067.8  
; PRIOR FILING DATE: 2000-01-17  
; PRIOR APPLICATION NUMBER: GB-0005699.4  
; PRIOR FILING DATE: 2000-03-09  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: SeqWin99, version 1.02

```
; SEQ ID NO 11
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-660-11

Query Match      94.4%; Score 752; DB 4; Length 797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 ADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETAD 80
Db 21 ADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETAD 80
Qy 81 GQLLLTVIERPTIGSLNITGAKMLQNDAIKNLESFGLAQSYFNQATLNQAVAGLKEEY 140
Db 81 GQLLLTVIERPTIGSLNITGAKMLQNDAIKNLESFGLAQSYFNQATLNQAVAGLKEEY 140
Qy 141 LGRGKLNIIQITPKVTKLARNRVDIDITIDEGSKAKITDIEFEGNOVYSDRKLRQMSLTE 200
Db 141 LGRGKLNIIQITPKVTKLARNRVDIDITIDEGSKAKITDIEFEGNOVYSDRKLRQMSLTE 200
Qy 201 GGIWTLTRSNOFNEQKFAQDMKVTDYQNNGYFDFRILDTDIQTNEDEKTKQITKITVH 260
Db 201 GGIWTLTRSNOFNEQKFAQDMKVTDYQNNGYFDFRILDTDIQTNEDEKTKQITKITVH 260
Qy 261 EGGRFRMGKVSIEGDTNEVPKAELEKLLTMKPGKWERQOMTAVLGEIQNRMGSAVAYS 320
Db 261 EGGRFRMGKVSIEGDTNEVPKAELEKLLTMKPGKWERQOMTAVLGEIQNRMGSAVAYS 320
Qy 321 EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVVRRELQMESAPYDTS 380
Db 321 EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVVRRELQMESAPYDTS 380
Qy 381 KLQRSKERVEVLLGYFDNVQFPAVLGTPDKVDLNMSLTERSTGSLDLSAGWQDTGLVM 440
Db 381 KLQRSKERVEVLLGYFDNVQFPAVLGTPDKVDLNMSLTERSTGSLDLSAGWQDTGLVM 440
Qy 441 SAGVSQDNLFQGTGSAALRASRSKTTLNGSLSPFTDPYFTADGVSGLGYDVYKAPDPKAS 500
Db 441 SAGVSQDNLFQGTGSAALRASRSKTTLNGSLSPFTDPYFTADGVSGLGYDVYKAPDPKAS 500
Qy 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHYADFIKKYKGTG 560
Db 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHYADFIKKYKGTG 560
Qy 561 TDGSFKGLYKGTGVGWRNKTDLSALWPTRGYLTGVNAEIALPGSKLQYYSATHNQWFFP 620
Db 561 TDGSFKGLYKGTGVGWRNKTDLSALWPTRGYLTGVNAEIALPGSKLQYYSATHNQWFFP 620
Qy 621 LSKTFTMLGGEVGIAGGYGRTKEIIPFFENFYGGGLGSRVGYESGTLGPKVYDEYGEKIS 680
Db 621 LSKTFTMLGGEVGIAGGYGRTKEIIPFFENFYGGGLGSRVGYESGTLGPKVYDEYGEKIS 680
Qy 681 YGKNKANVSAELLFPMPGAKDARTVRLSLFADAGSVWDGKTYDDNSSSATGGRVQNIYG 740
Db 681 YGKNKANVSAELLFPMPGAKDARTVRLSLFADAGSVWDGKTYDDNSSSATGGRVQNIYG 740
Qy 741 AGNTHKSTFTNELRYSGAGVATWLSPLGPMKF 772
Db 741 AGNTHKSTFTNELRYSGAGVATWLSPLGPMKF 772

RESULT 5
US-10-320-800-6
; Sequence 6, Application US/10320800
; Publication No. US20030215469A1
; GENERAL INFORMATION:
; APPLICANT: ROBINSON, ANDREW
; APPLICANT: GORRINGE, ANDREW
; APPLICANT: HUDSON, MICHAEL
; APPLICANT: REDDIN, KAREN
; TITLE OF INVENTION: MULTICOMPONENT MENINGOCOCCAL VACCINE
```

```
; FILE REFERENCE: 1581.0790001
; CURRENT APPLICATION NUMBER: US/10/320,800
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: PCT/GB99/03626
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-320-800-6

Query Match      94.4%; Score 752; DB 4; Length 797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 ADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETAD 80
Db 21 ADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETAD 80
Qy 81 GQLLLTVIERPTIGSLNITGAKMLQNDAIKNLESFGLAQSYFNQATLNQAVAGLKEEY 140
Db 81 GQLLLTVIERPTIGSLNITGAKMLQNDAIKNLESFGLAQSYFNQATLNQAVAGLKEEY 140
Qy 141 LGRGKLNIIQITPKVTKLARNRVDIDITIDEGSKAKITDIEFEGNOVYSDRKLRQMSLTE 200
Db 141 LGRGKLNIIQITPKVTKLARNRVDIDITIDEGSKAKITDIEFEGNOVYSDRKLRQMSLTE 200
Qy 201 GGIWTLTRSNOFNEQKFAQDMKVTDYQNNGYFDFRILDTDIQTNEDEKTKQITKITVH 260
Db 201 GGIWTLTRSNOFNEQKFAQDMKVTDYQNNGYFDFRILDTDIQTNEDEKTKQITKITVH 260
Qy 261 EGGRFRMGKVSIEGDTNEVPKAELEKLLTMKPGKWERQOMTAVLGEIQNRMGSAVAYS 320
Db 261 EGGRFRMGKVSIEGDTNEVPKAELEKLLTMKPGKWERQOMTAVLGEIQNRMGSAVAYS 320
Qy 321 EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVVRRELQMESAPYDTS 380
Db 321 EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVVRRELQMESAPYDTS 380
Qy 381 KLQRSKERVEVLLGYFDNVQFPAVLGTPDKVDLNMSLTERSTGSLDLSAGWQDTGLVM 440
Db 381 KLQRSKERVEVLLGYFDNVQFPAVLGTPDKVDLNMSLTERSTGSLDLSAGWQDTGLVM 440
Qy 441 SAGVSQDNLFQGTGSAALRASRSKTTLNGSLSPFTDPYFTADGVSGLGYDVYKAPDPKAS 500
Db 441 SAGVSQDNLFQGTGSAALRASRSKTTLNGSLSPFTDPYFTADGVSGLGYDVYKAPDPKAS 500
Qy 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHYADFIKKYKGTG 560
Db 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHYADFIKKYKGTG 560
Qy 561 TDGSFKGLYKGTGVGWRNKTDLSALWPTRGYLTGVNAEIALPGSKLQYYSATHNQWFFP 620
Db 561 TDGSFKGLYKGTGVGWRNKTDLSALWPTRGYLTGVNAEIALPGSKLQYYSATHNQWFFP 620
Qy 621 LSKTFTMLGGEVGIAGGYGRTKEIIPFFENFYGGGLGSRVGYESGTLGPKVYDEYGEKIS 680
Db 621 LSKTFTMLGGEVGIAGGYGRTKEIIPFFENFYGGGLGSRVGYESGTLGPKVYDEYGEKIS 680
Qy 681 YGKNKANVSAELLFPMPGAKDARTVRLSLFADAGSVWDGKTYDDNSSSATGGRVQNIYG 740
Db 681 YGKNKANVSAELLFPMPGAKDARTVRLSLFADAGSVWDGKTYDDNSSSATGGRVQNIYG 740
Qy 741 AGNTHKSTFTNELRYSGAGVATWLSPLGPMKF 772
Db 741 AGNTHKSTFTNELRYSGAGVATWLSPLGPMKF 772

RESULT 6
US-10-181-600-3
; Sequence 3, Application US/10181600
```





```
Qy 681 YGNKKANVSALLFPMPGAKDARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIYG 740
Db 681 YGNKKANVSALLFPMPGAKDARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIYG 740
Qy 741 AGNTHKSTFTNELRYSAGGAVTWLSPGPMKF 772
Db 741 AGNTHKSTFTNELRYSAGGAVTWLSPGPMKF 772

RESULT 8
US-10-988-943-7
; Sequence 7, Application US/10988943
; Publication No. US20050176085A1
; GENERAL INFORMATION:
; APPLICANT: Center for Genetic Engineering and Biotechnology
; TITLE OF INVENTION: METHOD OF SELECTIVE PEPTIDE ISOLATION FOR THE
; TITLE OF INVENTION: IDENTIFICATION AND QUANTITATIVE ANALYSIS OF PROTEINS IN
; TITLE OF INVENTION: COMPLEX MIXTURES.
; FILE REFERENCE: Proteomics CU2003-269
; CURRENT APPLICATION NUMBER: US/10/988,943
; CURRENT FILING DATE: 2004-11-15
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis (group B)
US-10-988-943-7

Query Match 94.4%; Score 752; DB 5; Length 797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 ADFTIQDIRVEGLQRTPESTVFVNLVVKVGDYNDTHGSAIIKSLYATGFFDDVRVETAD 80
Db 21 ADFTIQDIRVEGLQRTPESTVFVNLVVKVGDYNDTHGSAIIKSLYATGFFDDVRVETAD 80
Qy 81 GQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSYFNQATLNOAVAGLKEEY 140
Db 81 GQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSYFNQATLNOAVAGLKEEY 140
Qy 141 LGRGKLNIOITPKVTKLARNRVDITIDEGKSAKITDIEFEGNQVYSDRKLQMSLSTE 200
Db 141 LGRGKLNIOITPKVTKLARNRVDITIDEGKSAKITDIEFEGNQVYSDRKLQMSLSTE 200
Qy 201 GGIWTWLTNRNQNEQFAQDMKVTDIFYQNGYFDFRILDTDIQTNEDTKQTIKITVH 260
Db 201 GGIWTWLTNRNQNEQFAQDMKVTDIFYQNGYFDFRILDTDIQTNEDTKQTIKITVH 260
Qy 261 EGGFRFGKVSIEGDTNEVPKAELEKLLTMKPGKWERQMTAVLGEIQNRMSAGYAYS 320
Db 261 EGGFRFGKVSIEGDTNEVPKAELEKLLTMKPGKWERQMTAVLGEIQNRMSAGYAYS 320
Qy 321 EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVVRRELQMESAPYDTS 380
Db 321 EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVVRRELQMESAPYDTS 380
Qy 381 KLQSKERVLLGYFDNVQFQDAVPLAGTDPKVDLNMSLTERSTGSLDLSAGVQDITGLVM 440
Db 381 KLQSKERVLLGYFDNVQFQDAVPLAGTDPKVDLNMSLTERSTGSLDLSAGVQDITGLVM 440
Qy 441 SAGVSQNLFGTGKSAALRASRSKTTLNGSLSFDPDYPFTADGVSGLGYDVYVKAFDPRKAS 500
Db 441 SAGVSQNLFGTGKSAALRASRSKTTLNGSLSFDPDYPFTADGVSGLGYDVYVKAFDPRKAS 500
Qy 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYKNKAPHYADFIKKYKGTG 560
Db 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYKNKAPHYADFIKKYKGTG 560
Qy 561 TDGSKFGWLYKGTGVGGRNKTDSALWPTRGYLTGCVNAEIALPGSKLOYYSATHNQWTFPP 620
Db 561 TDGSKFGWLYKGTGVGGRNKTDSALWPTRGYLTGCVNAEIALPGSKLOYYSATHNQWTFPP 620
```

```
Qy 621 LSKTFTMLGGEVGIAGGYRTKEIPFFENFYGGGLGSVRGYESGTLGPKVYDEYGEKIS 680
Db 621 LSKTFTMLGGEVGIAGGYRTKEIPFFENFYGGGLGSVRGYESGTLGPKVYDEYGEKIS 680
Qy 681 YGNKKANVSALLFPMPGAKDARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIYG 740
Db 681 YGNKKANVSALLFPMPGAKDARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIYG 740
Qy 741 AGNTHKSTFTNELRYSAGGAVTWLSPGPMKF 772
Db 741 AGNTHKSTFTNELRYSAGGAVTWLSPGPMKF 772

RESULT 9
US-10-181-660-5
; Sequence 5, Application US/10181660
; Publication No. US20030027097A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181,660
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 5
; LENGTH: 776
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-660-5

Query Match 94.2%; Score 751; DB 4; Length 776;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 751; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 DFTIQDIRVEGLQRTPESTVFVNLVVKVGDYNDTHGSAIIKSLYATGFFDDVRVETADG 81
Db 1 DFTIQDIRVEGLQRTPESTVFVNLVVKVGDYNDTHGSAIIKSLYATGFFDDVRVETADG 60
Qy 82 QLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSYFNQATLNOAVAGLKEEYL 141
Db 61 QLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSYFNQATLNOAVAGLKEEYL 120
Qy 142 GRGKLNIOITPKVTKLARNRVDITIDEGKSAKITDIEFEGNQVYSDRKLQMSLSTE 201
Db 121 GRGKLNIOITPKVTKLARNRVDITIDEGKSAKITDIEFEGNQVYSDRKLQMSLSTE 180
Qy 202 GIWTLTNRNQNEQFAQDMKVTDIFYQNGYFDFRILDTDIQTNEDTKQTIKITVHE 261
Db 181 GIWTLTNRNQNEQFAQDMKVTDIFYQNGYFDFRILDTDIQTNEDTKQTIKITVHE 240
Qy 262 GGRFRFGKVSIEGDTNEVPKAELEKLLTMKPGKWERQMTAVLGEIQNRMSAGYAYS 321
Db 241 GGRFRFGKVSIEGDTNEVPKAELEKLLTMKPGKWERQMTAVLGEIQNRMSAGYAYS 300
Qy 322 EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVVRRELQMESAPYDTSK 381
Db 301 EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVVRRELQMESAPYDTSK 360
Qy 382 LQSKERVLLGYFDNVQFQDAVPLAGTDPKVDLNMSLTERSTGSLDLSAGVQDITGLVMS 441
Db 361 LQSKERVLLGYFDNVQFQDAVPLAGTDPKVDLNMSLTERSTGSLDLSAGVQDITGLVMS 420
Qy 442 AGVSQNLFGTGKSAALRASRSKTTLNGSLSFDPDYPFTADGVSGLGYDVYVKAFDPRKAST 501
Db 421 AGVSQNLFGTGKSAALRASRSKTTLNGSLSFDPDYPFTADGVSGLGYDVYVKAFDPRKAST 480
Qy 502 SIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYKNKAPHYADFIKKYKGTGDT 561
```

```
Db 481 SIKQYKTTTACAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHVADFIKKYKTKDGT 540
Qy 562 DGSFKGWLKGTGWRNKTDLSALWPRGRYLTGNABIALPGSKLOYYSATHNQTFWFFPL 621
Db 541 DGSFKGWLKGTGWRNKTDLSALWPRGRYLTGNABIALPGSKLOYYSATHNQTFWFFPL 600
Qy 622 SKTFTMLGGEVGIAGGYGRTKETIPFFENFYGGGLGSRVGESEGTGLPKVYDEYGEKISY 681
Db 601 SKTFTMLGGEVGIAGGYGRTKETIPFFENFYGGGLGSRVGESEGTGLPKVYDEYGEKISY 660
Qy 682 GGNKKANVSALLFPMPGAKDARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVONIYGA 741
Db 661 GGNKKANVSALLFPMPGAKDARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVONIYGA 720
Qy 742 GNTHKSTFTNELRYSGAGAVTWLSPGPMKF 772
Db 721 GNTHKSTFTNELRYSGAGAVTWLSPGPMKF 751

RESULT 10
US-10-181-660-13
; Sequence 13, Application US/10181660
; Publication No. US20030027097A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181,660
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Seqwin99, version 1.02
; SEQ ID NO 13
; TYPE: PRT
; LENGTH: 776
; ORGANISM: Neisseria meningitidis
US-10-181-660-13

Query Match 94.2%; Score 751; DB 4; Length 776;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 751; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 DFTIODIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIKSLVATGFFDDRVVETADG 81
Db 1 DFTIODIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIKSLVATGFFDDRVVETADG 60
Qy 82 QLLLTVIERPTIGSLNITGAKMLONDAIKKNLESEGLAQSYFNOATLNQAVAGLKEEYL 141
Db 61 QLLLTVIERPTIGSLNITGAKMLONDAIKKNLESEGLAQSYFNOATLNQAVAGLKEEYL 120
Qy 142 GRGKLNIIQITPKVTKLARNRVDITIDEGSAKITDIEFEGNOVYSDRKLQMSLTGEG 201
Db 121 GRGKLNIIQITPKVTKLARNRVDITIDEGSAKITDIEFEGNOVYSDRKLQMSLTGEG 180
Qy 202 GIWTLTRSNQNEQKFAQDMKEKVTDFYQNNGYFDFRILDTDIQTNEDTKTIIKITVHE 261
Db 181 GIWTLTRSNQNEQKFAQDMKEKVTDFYQNNGYFDFRILDTDIQTNEDTKTIIKITVHE 240
Qy 262 GGRFRMGKVSIEGDTNEVPKAELEKLLTWKPGKWERQOMTAVLGIEIQNRMSAGYAYSE 321
Db 241 GGRFRMGKVSIEGDTNEVPKAELEKLLTWKPGKWERQOMTAVLGIEIQNRMSAGYAYSE 300
Qy 322 ISVQPLPNAETKTVDFVLHIEPGRKIYVNEIHTGNKTRDEVRRRELQMESAPYDTSK 381
Db 301 ISVQPLPNAETKTVDFVLHIEPGRKIYVNEIHTGNKTRDEVRRRELQMESAPYDTSK 360
Qy 382 LQSKSERVELLYGFDVNVQDVAFLAGTDPKVDLNMSLTERSTGSLDSAGWQDVLNMS 441
Db 361 LQSKSERVELLYGFDVNVQDVAFLAGTDPKVDLNMSLTERSTGSLDSAGWQDVLNMS 420
```

```
Qy 442 AGVSQDNLFOTGSAALRASRSKTTTLNGSLSFDTDPYFTADGVSLGYDVYKKAEDPRKAST 501
Db 421 AGVSQDNLFOTGSAALRASRSKTTTLNGSLSFDTDPYFTADGVSLGYDVYKKAEDPRKAST 480
Qy 502 SIKQYKTTTACAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHVADFIKKYKTKDGT 561
Db 481 SIKQYKTTTACAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHVADFIKKYKTKDGT 540
Qy 562 DGSFKGWLKGTGWRNKTDLSALWPRGRYLTGNABIALPGSKLOYYSATHNQTFWFFPL 621
Db 541 DGSFKGWLKGTGWRNKTDLSALWPRGRYLTGNABIALPGSKLOYYSATHNQTFWFFPL 600
Qy 622 SKTFTMLGGEVGIAGGYGRTKETIPFFENFYGGGLGSRVGESEGTGLPKVYDEYGEKISY 681
Db 601 SKTFTMLGGEVGIAGGYGRTKETIPFFENFYGGGLGSRVGESEGTGLPKVYDEYGEKISY 660
Qy 682 GGNKKANVSALLFPMPGAKDARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVONIYGA 741
Db 661 GGNKKANVSALLFPMPGAKDARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVONIYGA 720
Qy 742 GNTHKSTFTNELRYSGAGAVTWLSPGPMKF 772
Db 721 GNTHKSTFTNELRYSGAGAVTWLSPGPMKF 751

RESULT 11
US-10-181-600-5
; Sequence 5, Application US/10181600
; Publication No. US20040249125A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181,600
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Seqwin99, version 1.02
; SEQ ID NO 5
; LENGTH: 776
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-600-5

Query Match 94.2%; Score 751; DB 5; Length 776;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 751; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 DFTIODIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIKSLVATGFFDDRVVETADG 81
Db 1 DFTIODIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIKSLVATGFFDDRVVETADG 60
Qy 82 QLLLTVIERPTIGSLNITGAKMLONDAIKKNLESEGLAQSYFNOATLNQAVAGLKEEYL 141
Db 61 QLLLTVIERPTIGSLNITGAKMLONDAIKKNLESEGLAQSYFNOATLNQAVAGLKEEYL 120
Qy 142 GRGKLNIIQITPKVTKLARNRVDITIDEGSAKITDIEFEGNOVYSDRKLQMSLTGEG 201
Db 121 GRGKLNIIQITPKVTKLARNRVDITIDEGSAKITDIEFEGNOVYSDRKLQMSLTGEG 180
Qy 202 GIWTLTRSNQNEQKFAQDMKEKVTDFYQNNGYFDFRILDTDIQTNEDTKTIIKITVHE 261
Db 181 GIWTLTRSNQNEQKFAQDMKEKVTDFYQNNGYFDFRILDTDIQTNEDTKTIIKITVHE 240
Qy 262 GGRFRMGKVSIEGDTNEVPKAELEKLLTWKPGKWERQOMTAVLGIEIQNRMSAGYAYSE 321
Db 241 GGRFRMGKVSIEGDTNEVPKAELEKLLTWKPGKWERQOMTAVLGIEIQNRMSAGYAYSE 300
Qy 322 ISVQPLPNAETKTVDFVLHIEPGRKIYVNEIHTGNKTRDEVRRRELQMESAPYDTSK 381
```

```
Db 301 ISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHITGNKTRDEVVRRELQMESAPYDTSK 360
Qy 382 LQSKERVELLGYFDNVQFQDAVPLAGTDPDKVDLNMSLTERSTGSLDLSAGWQDTGLVMS 441
Db 361 LQSKERVELLGYFDNVQFQDAVPLAGTDPDKVDLNMSLTERSTGSLDLSAGWQDTGLVMS 420
Qy 442 AGVSQDNLFGTGKSAALRASRSKTTLLNGSLSFDPYFTADGVSIGYDVYKAFDPRKAST 501
Db 421 AGVSQDNLFGTGKSAALRASRSKTTLLNGSLSFDPYFTADGVSIGYDVYKAFDPRKAST 480
Qy 502 SIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHVADFIKKYKTDGT 561
Db 481 SIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHVADFIKKYKTDGT 540
Qy 562 DGSFKGWLKGTGVMGRNKTDLSALWPTRGYLTGVNAEIALPGSKLQYYSATHNQTFWFFPL 621
Db 541 DGSFKGWLKGTGVMGRNKTDLSALWPTRGYLTGVNAEIALPGSKLQYYSATHNQTFWFFPL 600
Qy 622 SKTFTLLMGGEVGTAGGYGRTKEIPFPENFYGGGLGSRVGYESGTLGPKYVDEYGEKISY 681
Db 601 SKTFTLLMGGEVGTAGGYGRTKEIPFPENFYGGGLGSRVGYESGTLGPKYVDEYGEKISY 660
Qy 682 GGNKANVSAELLFPMPGAADARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIYGA 741
Db 661 GGNKANVSAELLFPMPGAADARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIYGA 720
Qy 742 GNTHKSTFTNELRYSAGGAVTWLSPGLPMKF 772
Db 721 GNTHKSTFTNELRYSAGGAVTWLSPGLPMKF 751

RESULT 12
US-10-181-600-13
; Sequence 13, Application US/10181600
; Publication No. US20040249125A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785W0
; CURRENT APPLICATION NUMBER: US/10/181.600
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 13
; LENGTH: 776
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-600-13
```

```
Query Match 94.2%; Score 751; DB 5; Length 776;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 751; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 22 DFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETADG 81
Db 1 DFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETADG 60
Qy 82 QLLLTVIERPTIGSLNITGAKMLQNDAIKKNLSEFGLAQSQYFQOATLNQAVAGLKEEYL 141
Db 61 QLLLTVIERPTIGSLNITGAKMLQNDAIKKNLSEFGLAQSQYFQOATLNQAVAGLKEEYL 120
Qy 142 GRGKLNQITPKVTKLARNRVDDIITIDEGSAKITIDIEPEGNQVYSDRKLQMSLTEG 201
Db 121 GRGKLNQITPKVTKLARNRVDDIITIDEGSAKITIDIEPEGNQVYSDRKLQMSLTEG 180
Qy 202 GIWTLWLRNSQFNQKPAQDMKEKVTDFYQNNGYFDFRILDTIDITNEDKTKQTIKIIVHE 261
Db 181 GIWTLWLRNSQFNQKPAQDMKEKVTDFYQNNGYFDFRILDTIDITNEDKTKQTIKIIVHE 240
```

```
Qy 262 GGRFRNGKVISIEGDTNEVPKAELEKLLTMKPGKMYERQOQMTAVLGEIQNRMGSAQYAYSE 321
Db 241 GGRFRNGKVISIEGDTNEVPKAELEKLLTMKPGKMYERQOQMTAVLGEIQNRMGSAQYAYSE 300
Qy 322 ISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHITGNKTRDEVVRRELQMESAPYDTSK 381
Db 301 ISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHITGNKTRDEVVRRELQMESAPYDTSK 360
Qy 382 LQSKERVELLGYFDNVQFQDAVPLAGTDPDKVDLNMSLTERSTGSLDLSAGWQDTGLVMS 441
Db 361 LQSKERVELLGYFDNVQFQDAVPLAGTDPDKVDLNMSLTERSTGSLDLSAGWQDTGLVMS 420
Qy 442 AGVSQDNLFGTGKSAALRASRSKTTLLNGSLSFDPYFTADGVSIGYDVYKAFDPRKAST 501
Db 421 AGVSQDNLFGTGKSAALRASRSKTTLLNGSLSFDPYFTADGVSIGYDVYKAFDPRKAST 480
Qy 502 SIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHVADFIKKYKTDGT 561
Db 481 SIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHVADFIKKYKTDGT 540
Qy 562 DGSFKGWLKGTGVMGRNKTDLSALWPTRGYLTGVNAEIALPGSKLQYYSATHNQTFWFFPL 621
Db 541 DGSFKGWLKGTGVMGRNKTDLSALWPTRGYLTGVNAEIALPGSKLQYYSATHNQTFWFFPL 600
Qy 622 SKTFTLLMGGEVGTAGGYGRTKEIPFPENFYGGGLGSRVGYESGTLGPKYVDEYGEKISY 681
Db 601 SKTFTLLMGGEVGTAGGYGRTKEIPFPENFYGGGLGSRVGYESGTLGPKYVDEYGEKISY 660
Qy 682 GGNKANVSAELLFPMPGAADARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIYGA 741
Db 661 GGNKANVSAELLFPMPGAADARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIYGA 720
Qy 742 GNTHKSTFTNELRYSAGGAVTWLSPGLPMKF 772
Db 721 GNTHKSTFTNELRYSAGGAVTWLSPGLPMKF 751

RESULT 13
US-10-181-660-7
; Sequence 7, Application US/10181660
; Publication No. US20030027097A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785W0
; CURRENT APPLICATION NUMBER: US/10/181.660
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7
; LENGTH: 792
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-181-660-7
```

```
Query Match 26.3%; Score 210; DB 4; Length 792;
Best Local Similarity 100.0%; Pred. No. 2e-199;
Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Db 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Qy 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLSEFGLAQ 120
Db 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLSEFGLAQ 120
Qy 121 SOYFNOATLNQAVAGLKEEYVGRGKLNQITPKVTKLARNRVDDIITIDEGSAKITIDIE 180
```

Db 121 SOYFNOATLNOAVAGLKEEYLGKLNLIQITPKVTKLARNRVDIDITDEGKSAKITDIE 180

Qy 181 PEGNOVSDRKLMRQMSLTEGGIWTWLTTRS 210

Db 181 PEGNOVSDRKLMRQMSLTEGGIWTWLTTRS 210

RESULT 14

US-10-181-600-7

; Sequence 7, Application US/10181600

; Publication No. US20040249125A1

; GENERAL INFORMATION:

; APPLICANT: CHIRON SpA

; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS

; FILE REFERENCE: P023785WO

; CURRENT APPLICATION NUMBER: US/10/181.600

; CURRENT FILING DATE: 2002-07-17

; PRIOR APPLICATION NUMBER: GB-0001067.8

; PRIOR FILING DATE: 2000-01-17

; PRIOR APPLICATION NUMBER: GB-0005699.4

; PRIOR FILING DATE: 2000-03-09

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: SeqWin99, version 1.02

; SEQ ID NO 7

; LENGTH: 792

; TYPE: PRT

; ORGANISM: Neisseria gonorrhoeae

US-10-181-600-7

Best Local Similarity 100.0%; Pred. No. 1.6e-178;

Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 DFTIQDIRVEGLQRTPESTVFVNYLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETADG 81

Db 1 DFTIQDIRVEGLQRTPESTVFVNYLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETADG 60

Qy 82 QLLLTWIERPTIGSLNITGAKMLQNDAIKKNLESFGLAOSQYFNQATLNOAVAGLKEEYL 141

Db 61 QLLLTWIERPTIGSLNITGAKMLQNDAIKKNLESFGLAOSQYFNQATLNOAVAGLKEEYL 120

Qy 142 GRKLNLIQITPKVTKLARNRVDIDITDEGKSAKITDIEFEGNQVYSDRKLMRQMSLTEG 201

Db 121 GRKLNLIQITPKVTKLARNRVDIDITDEGKSAKITDIEFEGNQVYSDRKLMRQMSLTEG 180

Qy 202 GIWTLTTRS 210

Db 181 GIWTLTTRS 189

Search completed: April 12, 2006, 16:38:15

Job time : 185 secs

Query Match 26.3%; Score 210; DB 5; Length 792;

Best Local Similarity 100.0%; Pred. No. 2e-199;

Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFVNYLPVKVGDYNDTHGSA 60

Db 1 MKLQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFVNYLPVKVGDYNDTHGSA 60

Qy 61 IIKSLYATGFFDDVRVETADGQLLLTWIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120

Db 61 IIKSLYATGFFDDVRVETADGQLLLTWIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120

Qy 121 SOYFNOATLNOAVAGLKEEYLGKLNLIQITPKVTKLARNRVDIDITDEGKSAKITDIE 180

Db 121 SOYFNOATLNOAVAGLKEEYLGKLNLIQITPKVTKLARNRVDIDITDEGKSAKITDIE 180

Qy 181 PEGNOVSDRKLMRQMSLTEGGIWTWLTTRS 210

Db 181 PEGNOVSDRKLMRQMSLTEGGIWTWLTTRS 210

RESULT 15

US-10-181-660-9

; Sequence 9, Application US/10181660

; Publication No. US20030027097A1

; GENERAL INFORMATION:

; APPLICANT: CHIRON SpA

; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS

; FILE REFERENCE: P023785WO

; CURRENT APPLICATION NUMBER: US/10/181.660

; CURRENT FILING DATE: 2003-03-31

; PRIOR APPLICATION NUMBER: GB-0001067.8

; PRIOR FILING DATE: 2000-01-17

; PRIOR APPLICATION NUMBER: GB-0005699.4

; PRIOR FILING DATE: 2000-03-09

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: SeqWin99, version 1.02

; SEQ ID NO 9

; LENGTH: 771

; TYPE: PRT

; ORGANISM: Neisseria gonorrhoeae

US-10-181-660-9

Query Match 23.7%; Score 189; DB 4; Length 771;

**This Page Blank (uspto)**